STIC Search Report
Biotech-Chem Library

USPTO

STIC Database Tracking Number: 96722

TO: Sheela Huff
Location: CM1/8B07/8E12
Art Unit: 1642
Sunday, June 22, 2003

Case Serial Number: 830811

From: Mary Jane Ruhl
Location: Biotech-Chem Library
CM1-6A06
Phone: 605-1155

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Search Notes

NO 0117557

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Search and Information
Resources Administration

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:05:14 ; Search time 1915 Seconds
                   (without alignments)
                   273.551 Million cell updates/sec

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GenCore version 5.1.6

Title: US-09-830-811-1
Perfect score: 18
Sequence: 1 ggcggcttgtaaacagta 18
Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 1455140287B residues

Total number of hits satisfying chosen parameters: 4109280

Post-processing: Minimum Match 0%
                   Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Listing first 45 summaries

Database : GenEmbl:*

No.	Database
1:	gb_ba:*
2:	gb_htg:*
3:	gb_in:*
4:	gb_om:*
5:	gb_ov:*
6:	gb_pat:*
7:	gb_ph:*
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29:	em_vrl:*
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32:	em_htg_inv:*
33:	em_htg_other:*
34:	em_htg_mus:*
35:	em_htg_pln:*
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37:	em_htg_mam:*
38:	em_htg_vrt:*
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40:	em_htgo_hum:*
40:	em_htgo_mus:*
41:	em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1	c	18	100.0	2625	6	A83536	A83536 Sequence 1
2	c	18	100.0	2625	6	AX093786	AX093786 Sequence 57
3	c	18	100.0	2625	6	I34433	I34433 Sequence 57
4	c	18	100.0	2625	6	I46831	I46831 Sequence 51
5	c	18	100.0	2625	6	I55100	I55100 Sequence 51
6	c	18	100.0	3440	6	L34056	L34056 Homo sapi
7	c	18	100.0	3661	6	HUMCA11A	HUMCA11A Human mRNA
8	c	18	100.0	3661	6	BC013609	BC013609 Homo sapi
9	c	18	100.0	3712	6	HUMOSF4A	HUMOSF4A Homo sapi
10	c	18	100.0	3712	6	AR034822	AR034822 Sequence
11	c	18	100.0	3712	6	E07382	E07382 cDNA encodi
12	c	18	100.0	3867	6	D21255	D21254 Human mRNA
13	c	18	100.0	3914	6	AR034823	AR034823 Sequence
14	c	18	100.0	3914	6	HUMOSF4B	HUMOSF4B Homo sapi
15	c	18	100.0	153888	9	E07383	E07383 cDNA encod1
16	c	18	100.0	189894	2	AC068656	AC068656 Homo sapi
17	c	18	100.0	194690	9	AC025763	AC025763 Homo sapi
18	c	16.4	91.1	3180	10	MUSC11	MUSC11 Mouse mRNA
19	c	16.4	91.1	3489	10	MUSOSF4	MUSOSF4 Mouse mRNA
20	c	16.4	91.1	3581	6	AR034821	AR034821 Sequence
21	c	16.4	91.1	3581	6	E07381	E07381 cDNA encodi
22	c	16.4	91.1	4127	6	AX306074	AX306074 Sequence
23	c	16.4	91.1	4127	10	MMCADL	MMCADL
24	c	16.4	91.1	64849	9	AL138714	AL138714 Human DNA
25	c	16.4	91.1	106376	9	AC113037	AC113037 Mus muscu
26	c	16.4	91.1	118327	9	HSD48613	HSD48613 Human DNA
27	c	16.4	91.1	163192	2	AC123048	AC123048 Mus muscu
28	c	16.4	91.1	170453	2	AC006600	AC006600 Homo sapi
29	c	16.4	91.1	173556	2	AC074388	AC074388 Homo sapi
30	c	16.4	91.1	176625	2	AC015977	AC015977 Homo sapi
31	c	16.4	91.1	178549	2	AL590312	AL590312 Homo sapi
32	c	16.4	91.1	205594	2	AC109962	AC109962 Rattus no
33	c	16.4	91.1	207212	2	AL355373	AL355373 Homo sapi
34	c	16	88.9	4520	8	AL671876	AL671876 Mus muscu
35	c	16.4	91.1	345	9	D88669	D88669 Bryopsis c1
36	c	15.4	85.6	1206	9	AK027308	AK027308 Homo sapi
37	c	15.4	85.6	1522	6	BC001611	BC001611 Homo sapi
38	c	15.4	85.6	1695	10	RNU56936	U56936 Rattus norv
39	c	15.4	85.6	2137	9	AF213969	AF213969 Homo sapi
40	c	15.4	85.6	2210	9	HSA271881	AJ271881 Homo sapi
41	c	15.4	85.6	2213	9	AF152604	AF152604 Homo sapi
42	c	15.4	85.6	2307	1	ARI16594	AR116594 Sequence
43	c	15.4	85.6	3268	1	AF269352	AF269352 Staphyloc
44	c	15.4	85.6	3268	6	AX144672	AX144672 Sequence
45	.	15.4	85.6	10058	1	AE001050	AE001050 Archaeogl

ALIGNMENTS

RESULT 1
A83536/c
LOCUS   A83536   2625 bp   DNA   linear   PAT 21-JAN-2000
DEFINITION Sequence 1 from Patent WO9849560.
ACCESSION   A83536
VERSION   A83536.1 GI:6732796
KEYWORDS   .
SOURCE   unidentified.
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 2625)
  AUTHORS   Maccalman,C.D. and Stephenson,M.D.
  TITLE   CADHERIN-11 AS AN INDICATOR OF VIABLE PREGNANCY
  JOURNAL   Patent: WO 9849560-A 1 05-NOV-1998;
            MACCALMAN COLIN D (CA); STEPHENSON MARY D (CA)

FEATURES
  source   Location/Qualifiers
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                /organism="unidentified"
                /db_xref="taxon:32644"
BASE COUNT   730 a   661 c   675 g   559 t
ORIGIN

Qy   1 GGCGGGCTTGTAAACAGTA 18
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Db   185 GGCGGGCTTGTAAACAGTA 168

RESULT 2
LOCUS   AX093786   2625 bp   DNA   linear   PAT 30-MAR-2001
DEFINITION Sequence 1 from Patent WO0117557.
ACCESSION   AX093786
VERSION   AX093786.1 GI:13510049
KEYWORDS
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2625)
AUTHORS   Brenner,M.B. and Valencia,X.
TITLE   Methods and compositions for treatment of inflammatory disease
            using cadherin-11 modulating agents
JOURNAL   Patent: WO 0117557-A1 15-MAR-2001;
            THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
FEATURES   Location/Qualifiers
     source   1..2625
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /protein_id="CAC35421.1"
                     /db_xref="GI:13510050"
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                     HETYHANVPERSNVGTSVIQVTASDADDPTYGNSAKLVYSILEGQPYFSVEAQTGIIR
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                     VSEAAVPGEEVGRVKAKPDIGENGLVTYNIVDGDGMESFEITIDYETQEGVIKLKKP
                     VDFETERAYSLKVEAANVHIDPKFISNGPFKDVTVKISVEDADEPPMFLAPSYIHEV
                     QENAAAGTVVGRVHAKDPDAANSPIRISIDRIFDLDRFFTINPEDGFIKTTKPLDREE
                     TAWNINITVFAAEIHNRHQEAQVPVAIRVLDVNDNAPKFPAAPYEGFICESDQTKPLSNQ
                     PIVTISADDKDDTFANGPRPIFSLPPEIIHNPNTVRDNRDNTAGVYARRGFSROKQD
                     LYLLPIVISDGGIPPMSSTNTLTIKVCGGDVNGALLSCNAEAYILNAGLSTGALIAIL
                     ACIVILLIVIVLFVTLRRQKKEPLIVFEEEDVRENIIITYDDEGGGEDTEAFDIATLQ
                     NPDGINGFIPRKIDIKPEYQYMPRPGLRPAPNSVDVDDFINTRIQEADNDPTAPPYDSI
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BASE COUNT   730 a   661 c   675 g   559 t
ORIGIN

Qy   1 GGCGGGCTTGTAAACAGTA 18
          ||||||||||||||||||||
Db   185 GGCGGGCTTGTAAACAGTA 168

RESULT 3
LOCUS   I34433
DEFINITION Sequence 57 from patent US 5597725.
ACCESSION   I34433
VERSION   I34433.1 GI:1825224
KEYWORDS
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2625)
AUTHORS   Suzuki,S.
TITLE   Cadherin-specific antibodies and hybridoma cell lines
JOURNAL   Patent: US 5597725-A 57 28-JAN-1997;
FEATURES   Location/Qualifiers
     source   1..2625
                     /organism="unknown"
                     Location/Qualifiers
BASE COUNT   730 a   661 c   675 g   559 t
ORIGIN

Query Match   100.0%;   Score 18;   DB 6;   Length 2625;
Best Local Similarity 100.0%;   Pred. No. 41;
Matches 18;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 GGCGGGCTTGTAAACAGTA 18
          ||||||||||||||||||||
Db   185 GGCGGGCTTGTAAACAGTA 168

RESULT 4
LOCUS   I46831   2625 bp   DNA   linear   PAT 07-OCT-1997
DEFINITION Sequence 51 from patent US 5639634.
ACCESSION   I46831
VERSION   I46831.1 GI:2470796
KEYWORDS
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2625)
AUTHORS   Suzuki,S.
TITLE   Cadherin polynucleotides
JOURNAL   Patent: US 5639634-A 51 17-JUN-1997;
FEATURES   Location/Qualifiers
     source   1..2625
                     /organism="unknown"
                     Location/Qualifiers
BASE COUNT   730 a   661 c   675 g   559 t
ORIGIN

Query Match   100.0%;   Score 18;   DB 6;   Length 2625;
Best Local Similarity 100.0%;   Pred. No. 41;
Matches 18;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 GGCGGGCTTGTAAACAGTA 18
          ||||||||||||||||||||
Db   185 GGCGGGCTTGTAAACAGTA 168

RESULT 5
LOCUS   I55100   2625 bp   DNA   linear   PAT 07-OCT-1997
DEFINITION Sequence 57 from patent US 5645250.
ACCESSION   I55100
VERSION   I55100.1 GI:2476303
KEYWORDS
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2625)
AUTHORS   Suzuki,S.
TITLE   Cadherin polypeptides
JOURNAL   Patent: US 5645250-A 57 08-JUL-1997;
FEATURES   Location/Qualifiers
     source   1..2625
                     /organism="unknown"
                     Location/Qualifiers
BASE COUNT   730 a   661 c   675 g   559 t
ORIGIN

RESULT 6

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Qy          Query Match                    100.0%;                Score 18;  DB 6;   Length 2625;
            Best Local Similarity          100.0%;                Pred. No. 41;
            Matches   18;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy          1 GGCCGGCTTGTAAACAGTA 18
              ||||||||||||||||||
Db          185 GGCCGGCTTGTAAACAGTA 168
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LOCUS   HUMCA11A   2625 bp   mRNA   linear   PRI 29-JUN-1994
DEFINITION   Homo sapiens cadherin-11 mRNA, complete cds.
ACCESSION   L34056
VERSION   L34056.1 GI:506403
KEYWORDS   cadherin-11.
SOURCE   Homo sapiens fetus brain cDNA to mRNA.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2625)
  AUTHORS   Suzuki,S., Sano,K. and Tanihara,H.
  TITLE   Diversity of the cadherin family: evidence for eight new cadherins
             in nervous tissue
  JOURNAL   Cell Regul. 2 (4), 261-270 (1991)
  MEDLINE   91283540
   PUBMED   2059658
REFERENCE   2 (bases 1 to 2625)
  AUTHORS   Tanihara,H., Sano,K., Helmark,R.L., St.John,T. and Suzuki,S.
  TITLE   Cloning of five cadherins clarifies characteristic features of
             cadherin extracellular domain and provides further evidence for two
             structurally different types of cadherin
  JOURNAL   Cell Adhesion Commun. 2, 15-26 (1994)
FEATURES   Location/Qualifiers
     source   1..2625
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                     /db_xref="taxon:9606"
                     /tissue_type="brain"
                     /dev_stage="fetus"
     CDS   156..2546
                     /function="cell adhesion"
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                     /product="cadherin-11"
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BASE COUNT   730 a   661 c   675 g   559 t
ORIGIN
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Qy          1 GGCCGGCTTGTAAACAGTA 18
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Db          185 GGCCGGCTTGTAAACAGTA 168
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RESULT 7

LOCUS   BC013609   3440 bp   mRNA   linear   PRI 07-SEP-2001
DEFINITION   Homo sapiens, clone MGC:17193 IMAGE:4183901, mRNA, complete cds.
ACCESSION   BC013609
VERSION   BC013609.1 GI:15488965
KEYWORDS   MGC.
SOURCE   Homo sapiens.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3440)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (04-SEP-2001) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA
COMMENT   Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Baylor College of Medicine Human Genome
             Sequencing Center
             Center code: BCM-HGSC
             Web site: http://www.hgsc.bcm.tmc.edu/cdna/
             Contact: villalon@bcm.tmc.edu.
             Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
             A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
             Muzny,D.M., Gibbs,R.A.
             NIH-MGC Project URL: http://mgc.nci.nih.gov
REMARK   Clone distribution: MGC clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Series: IRAK Plate: 12 Row: 1 Column: 11
             This clone was selected for full length sequencing because it
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FEATURES   Location/Qualifiers
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     CDS   175..2565
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                     TALPNMDREAKEEYHVVIQAKDMGGHMGGLSGTTKVITILTDVNDNPPKFPQRLYQMS
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BASE COUNT   1055 a   774 c   792 g   819 t
ORIGIN
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Qy          Query Match                    100.0%;                Score 18;  DB 9;   Length 3440;
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            Matches . 18;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
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RESULT 8

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Qy         1 GGCGGCTTGTAAACAGTA 18
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Db       204 GGCGGCTTGTAAACAGTA 187
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LOCUS   HUMOSF4A/c
DEFINITION   Human mRNA for OB-cadherin-1, complete cds.
ACCESSION   D21254
VERSION   D21254.1   GI:575577
KEYWORDS   osf-4; OB-cadherin-1.
SOURCE   Homo sapiens new born osteosarcoma cDNA to mRNA, clone:pKOT170.
ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (sites)
AUTHORS   Okazaki,M., Takeshita,S., Kawai,S., Kikuno,R., Tsujimura,A.,
                Kudo,A. and Amann,E.
TITLE   Molecular cloning and characterization of OB-cadherin, a new member
                of cadherin family expressed in osteoblasts
JOURNAL   J. Biol. Chem. 269 (16), 12092-12098 (1994)
MEDLINE   94216322
REFERENCE   2 (bases 1 to 3661)
AUTHORS   Kikuno,R.
TITLE   Direct Submission
JOURNAL   Submitted (21-OCT-1993) Reiko Kikuno, Hoechst Japan Ltd., Pharma
                Research Labs.; 1-3-2 Minami-dai, Kawagoe, Saitama 350-11, Japan
                (E-mail:rkikuno@ddbj.nig.ac.jp, Tel:0492-43-6149, Fax:0492-43-2479)
FEATURES   Location/Qualifiers
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                     ACIVILLVIVVLFVTLRRQKKEPLIVFEEEDVRENIITVDDGGGEEDTEAFDIATLQ
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BASE COUNT      1059 a     846 c     883 g     873 t
ORIGIN

RESULT 9

AR034822/c

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Qy         1 GGCGGCTTGTAAACAGTA 18
             |||||||||||||||||||
Db       471 GGCGGCTTGTAAACAGTA 454
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Query Match   100.0%; Score 18; DB 9; Length 3661;
Best Local Similarity 100.0%; Pred. No. 37;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

LOCUS   AR034822   3712 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION   Sequence 3 from patent US 5869638.
ACCESSION   AR034822
VERSION   AR034822.1   GI:5950427
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 3712)
  AUTHORS   Takeshita,S., Okazaki,M., Kawai,S., Tsujimura,A. and Amann,E.
  TITLE   Bone-related cadherin-like protein and process for its production
  JOURNAL   Patent: US 5869638-A 3 09-FEB-1999;
FEATURES   Location/Qualifiers
     source   1..3712
                     /organism="unknown"
BASE COUNT   1074 a   856 c   897 g   885 t
ORIGIN

RESULT 10

E07382/c

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Qy         1 GGCGGCTTGTAAACAGTA 18
             |||||||||||||||||||
Db       490 GGCGGCTTGTAAACAGTA 473
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Query Match   100.0%; Score 18; DB 6; Length 3712;
Best Local Similarity 100.0%; Pred. No. 37;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

LOCUS   E07382   3712 bp   RNA   linear   PAT 29-SEP-1997
DEFINITION   cDNA encoding human OSF-4.
ACCESSION   E07382
VERSION   E07382.1   GI:2175521
KEYWORDS   JP 1994122700-A/2.
SOURCE   Homo sapiens
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3712)
  AUTHORS   Takeshita,A., Okazaki,M., Kawai,S., Tsujimura,A. and Amann,E.
  TITLE   BONE-RELATED CADHERIN-LIKE PROTEIN AND ITS PRODUCTION
  JOURNAL   Patent: JP 1994122700-A 2 06-MAY-1994;
                HOECHST JAPAN LTD
COMMENT   OS   Homo sapiens (human)
                PN   JP 1994122700-A/2
                PD   06-MAY-1994
                PF   13-JUL-1993 JP 199317Z883
                PR   28-AUG-1992 JP 92P 230028
                PI   TAKESHITA ATSUSHI, OKAZAKI MAKOTO, KAWAI SHINJI, PI
                TSUJIMURA ATSUSHI;
                PI   AMAN EGON
                PC   C07K13/00,A61K37/02,A61K37/02,A61K39/395,A61K39/395,A61K49/00,
                PC   C07K15/14,
                PC   C12N15/12,C12P21/02,C12P21/08;
                CC   strandedness: Double;
                CC   topology: Linear;
                CC   hypothetical: No;
                CC   anti-sense: No;
FEATURES   Key   Location/Qualifiers
FH
FH
FT   source   1..3712
FT   /organism="Homo sapiens"
FT   /cell_type="primary bone cancer" FT
FT   /clone="pKOT161"
FT   5'UTR   1..460
FT   CDS   461..2851
FT   /product="Human OSF-4"
FT   3'UTR   2852..3712.
                     Location/Qualifiers
                     1..3712
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT   1074 a   856 c   897 g   885 t

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ORIGIN

RESULT 11
LOCUS        HUMOSF4B/c
DEFINITION   Human mRNA for OB-cadherin-2, complete cds.
ACCESSION    D21255
VERSION      D21255.1  GI:575578
KEYWORDS     osf-4; OB-cadherin-2.
SOURCE       Homo sapiens new born osteosarcoma cDNA to mRNA, clone:pKOT161.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (sites)
AUTHORS      Okazaki,M., Takeshita,S., Kawai,S., Kikuno,R., Tsujimura,A.,
             Kudo,A. and Amann,E.
TITLE        Molecular cloning and characterization of OB-cadherin, a new member
             of cadherin family expressed in osteoblasts
JOURNAL      J. Biol. Chem. 269 (16), 12092-12098 (1994)
MEDLINE      94216322
REFERENCE    2  (bases 1 to 3867)
AUTHORS      Kikuno,R.
TITLE        Direct Submission
JOURNAL      Submitted (21-OCT-1993) Reiko Kikuno, Hoechst Japan Ltd., Pharma
             Research Labs.; 1-3-2 Minami-dai, Kawagoe, Saitama 350-11, Japan
             (E-mail:rkikuno@ddbj.nig.ac.jp, Tel:0492-43-6149, Fax:0492-43-2479)
FEATURES             Location/Qualifiers
     source          1..3867
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="pKOT161"
                     /tissue_type="osteosarcoma"
                     /dev_stage="new born"
     gene            1..3867
                     /gene="osf-4"
     CDS             477..2558
                     /gene="osf-4"
                     /codon_start=1
                     /product="OB-cadherin-2"
                     /protein_id="BAA04799.1"
                     /db_xref="GI:1377895"
                     /translation="MKENYCLQAALVCLGMLCHSHAFAPERGHLRPSFHGHHEKGKE
                     GGVLQRSKRGWVWNQFFVIEEYTGPDVLGVRLHSDIDSGDGNIKYILSGEAGTFV
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                     HETYHANVPERSNVGTSVIQVTASDADDPTYGNSAKLVYSILEGQPYFPSVEAQTGIIR
                     TALPNMDREAKEYHVVIQAKDMGGHMGGLSGTTKVTITLTDVNDNPPKFPQSVYQIS
                     VSEAAVPGEEVGRVKAKDPDIGENGLVTYNIVDGDGMESFEITDYETQEGVIKLKKP
                     VDFETKRAYSLKVEAANVHIDPKFISNGPFKDTRTVKIAVEDADEPPMPLAPSYIHEV
                     QENAAAGTVVGRVHAKPDAAASPIRYSIDRHTDLDRFFTINPEDGFIKTTTKPLDREE
                     TAWLNIYFAAEIHNRHQEAKYPVAIRVLDVNDNAPKFAAAPYEGFICESDQTKPLSNQ
                     PIVTISADDKDDTPANGPRFIFSLPPEIIHNPNFTVRDNRDNTAGVYARRGGFSRQKQD
                     LYLLPIVISDGGIPPMSSTNTLTIRVCCDVNGALLSCNAEAYILNAGLSTGALIAIL
                     ACIVILLGCPSLMEPPSPREDMRLLYLGFQLMLFSYKVNRRCLLGVFIKLPFLYVV
                     ATESPTTLFSL".

BASE COUNT    1098 a    905 c    932 g    932 t
ORIGIN

Qy        1 GGCGGCTTGTAAACAGTA 18
            ||||||||||||||||||
Db      490 GGCGGCTTGTAAACAGTA 473
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```
RESULT 12
LOCUS        AR034823                 3914 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION   Sequence 5 from patent US 5869638.
ACCESSION    AR034823
VERSION      AR034823.1  GI:5950428
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 3914)
AUTHORS      Takeshita,S., Okazaki,M., Kawai,S., Tsujimura,A. and Amann,E.
TITLE        Bone-related cadherin-like protein and process for its production
JOURNAL      Patent: US 5869638-A 5 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1..3914
                     /organism="unknown"

BASE COUNT    1110 a    916 c    944 g    944 t
ORIGIN

Qy        1 GGCGGCTTGTAAACAGTA 18
            ||||||||||||||||||
Db      520 GGCGGCTTGTAAACAGTA 503
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```
RESULT 13
LOCUS        E07383                   3914 bp    RNA     linear   PAT 29-SEP-1997
DEFINITION   cDNA encoding human OSF-4.
ACCESSION    E07383
VERSION      E07383.1  GI:2175522
KEYWORDS     JP 1994122700-A/3.
SOURCE       Homo sapiens.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 3914)
AUTHORS      Takeshita,A., Okazaki,M., Kawai,S., Tsujimura,A. and Aman,E.
TITLE        BONE-RELATED CADHERIN-LIKE PROTEIN AND ITS PRODUCTION
JOURNAL      Patent: JP 1994122700-A 3 06-MAY-1994;
             HOECHST JAPAN LTD
COMMENT      OS   Homo sapiens (human)
             PN   JP 1994122700-A/3
             PD   06-MAY-1994
             PF   13-JUL-1993 JP 1993172883
             PR   28-AUG-1992 JP 92P 230028
             PI   TAKESHITA ATSUSHI, OKAZAKI MAKOTO, KAWAI SHINJI, PI
             TSUJIMURA ATSUSHI;
             PI   AMAN EGON
             PC   C07K13/00,A61K37/02,A61K37/02,A61K39/395,A61K39/395,A61K49/00,
             PC   C07K15/14,
             PC   C1N15/12,C12P21/02,C12P21/08;
             PC   strandedness: Double;
             CC   topology: Linear;
             CC   hypothetical: No;
             CC   anti-sense: No;
     Key             Location/Qualifiers
     source          1..3914
                     /organism='Homo sapiens'
                     /cell_type= primary bone cancer' FT
                     /clone='pKOT170'
     5'UTR           1..490
     CDS             491..2572
                     /product='Human OSF-4'
     3'UTR           2573..3914.

FEATURES             Location/Qualifiers
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BASE COUNT    1098 a    905 c    932 g    932 t
ORIGIN

Qy        1 GGCGGCTTGTAAACAGTA 18
            ||||||||||||||||||
Db      506 GGCGGCTTGTAAACAGTA 489
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Query Match   100.0%; Score 18; DB 6; Length 3712;
Best Local Similarity   100.0%;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Query Match   100.0%; Score 18; DB 9; Length 3867;
Best Local Similarity   100.0%; Pred. No. 37;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Query Match   100.0%; Score 18; DB 6; Length 3914;
Best Local Similarity   100.0%; Pred. No. 36;
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     source          1..3914
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                     /db_xref="taxon:9606"
BASE COUNT     1110 a    916 c    944 g    944 t
ORIGIN
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Query Match   100.0%; Score 18; DB 6; Length 3914;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        1 GGCGGCGTTGTAAACAGTA 18
            |||||||||||||||||||
Db      520 GGCGGCGTTGTAAACAGTA 503
```

RESULT 14
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LOCUS       AC010533              153588 bp    DNA     linear   PRI 28-NOV-2000
DEFINITION  Homo sapiens chromosome 16 clone RP11-22903, complete sequence.
ACCESSION   AC010533
VERSION     AC010533.6  GI:11386272
KEYWORDS    HTG.
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 153588)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 153588)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 153588)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Nov 28, 2000 this sequence version replaced gi:9256236.
            Draft Sequence Produced by DOE Joint Genome Institute
            http://www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.9% of Sequence;
            Estimated Total Number of Errors is 0.5.
            STS Content:
            WI-9802 G05424
            WI-2756 G03521.
FEATURES             Location/Qualifiers
     source          1..153588
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                     /db_xref="taxon:9606"
                     /chromosome="16"
                     /clone="RP11-22903"
BASE COUNT     48714 a    29627 c    29013 g    46234 t
ORIGIN
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Query Match   100.0%; Score 18; DB 9; Length 153588;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        1 GGCGGCGTTGTAAACAGTA 18
            |||||||||||||||||||
Db    13378 GGCGGCGTTGTAAACAGTA 133395
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RESULT 15
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LOCUS       AC068656              189894 bp    DNA     linear   HTG 20-JUL-2000
DEFINITION  Homo sapiens chromosome 16 clone CTA-186A5, WORKING DRAFT SEQUENCE,
            22 ordered pieces.
ACCESSION   AC068656
VERSION     AC068656.2  GI:9295747
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 189894)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Human Chromosome 16
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 189894)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAY-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jul 20, 2000 this sequence version replaced gi:7712105.
            ------Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            ------
            Project Information
            Center Project Name: 1258011
            Center clone name: CTF978SKA_186A5
            ------
            Summary Statistics
            Consensus quality: 177227 bases at least Q40
            Consensus quality: 185750 bases at least Q30
            Consensus quality: 187169 bases at least Q20
            Estimated Insert size: 171860; agarose-fp estimation
            Estimated insert size: 188894; agarose-fp estimation
            Quality coverage: 7.12 in Q20 bases; sum-of-contigs estimation
            Quality coverage: 6.48 in Q20 bases; sum-of-contigs estimation.
            NOTE: This is a 'working draft' sequence. It currently
          * consists of 22 contigs. Gaps between the contigs
          * are represented as runs of N. The order of the pieces
          * is believed to be correct as given, however the sizes
          * of the gaps between them are based on estimates that have
          * provided by the submittor.
          * This sequence will be replaced
          * by the finished sequence as soon as it is available and
          * the accession number will be preserved.
          *       1    1851: contig of 1851 bp in length
          *    1852    1851: gap of unknown length
          *    1952    1951: contig of 1980 bp in length
          *    3931    3931: gap of unknown length
          *    3932    4031: contig of 1677 bp in length
          *    4032    4031: gap of unknown length
          *    4494    4494: contig of 974 bp in length
          *    8625    8625: gap of unknown length
          *    8626    4399: contig of 4494 bp in length
          *   13024   13024: gap of unknown length
          *   13025   13124: contig of 1734 bp in length
          *   13124   13124: gap of unknown length
          *   13125    588: contig of 588 bp in length
          *   14159   14159: gap of unknown length
          *   14160    974: contig of 4399 bp in length
          *   14259   14259: gap of unknown length
          *   14260   1677: contig of 15901 bp in length
          *   15936   15936: gap of unknown length
          *   15937   15901: contig of 1035 bp in length
          *   16036   16036: gap of unknown length
          *   16037   1035: contig of 29696 bp in length
          *   17770   17770: gap of unknown length
          *   17771   29696: contig of 2629 bp in length
          *   17870   17870: gap of unknown length
          *   17871   2629: contig of 17616 bp in length
          *   18458   18458: gap of unknown length
          *   18459   17616: contig of 759 bp in length
          *   18558   18558: gap of unknown length
          *   18559    759: contig of 8198 bp in length
          *   34459   34459: gap of unknown length
          *   34460   15901: contig of unknown length
          *   34559   34559: gap of unknown length
          *   34560   1035: contig of unknown length
          *   35533   35533: gap of unknown length
          *   35534   29696: contig of unknown length
          *   35633   35633: gap of unknown length
          *   35634   2629: contig of unknown length
          *   53349   53349: gap of unknown length
          *   53350   17616: contig of unknown length
          *   53977   53977: gap of unknown length
          *   53978    759: contig of unknown length
          *   55774   55774: gap of unknown length
          *   55775    8198: contig of unknown length
          *   85874   85874: gap of unknown length
          *   85875   29696: contig of unknown length
          *   86633   86633: gap of unknown length
          *   86634    759: contig of unknown length
          *   86733   86733: gap of unknown length
          *   86734    8198: contig of unknown length
          *   94931   94931: gap of unknown length
          *   94932    8198: contig of unknown length
          *   95031   95031: gap of unknown length
```

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FEATURES             Location/Qualifiers
     source          1..189894
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="16"
                     /clone="CTA-186A5"
                     /clone_lib="CalTech human BAC library A"
BASE COUNT     59539 a    37380 c    36768 g    54101 t    2106 others
ORIGIN
     1..189894
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  *     95952     96051:  gap of unknown length
  *     96052    138398:  contig of 42347 bp in length
  *    138399    138498:  gap of unknown length
  *    138499    143968:  contig of 5470 bp in length
  *    143969    144068:  gap of unknown length
  *    144069    152768:  contig of 8700 bp in length
  *    152769    152868:  gap of unknown length
  *    152869    153842:  contig of 974 bp in length
  *    153843    153942:  gap of unknown length
  *    153943    166638:  contig of 12696 bp in length
  *    166639    166738:  gap of unknown length
  *    166739    189894:  contig of 23156 bp in length.
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Query Match                  100.0%;  Score 18;  DB 2;  Length 189894;
Best Local Similarity        100.0%;  Pred. No. 11;
Matches     18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGCGGGCTTGTAAACAGTA 18
            ||||||||||||||||||
Db    81209 GGCGGGCTTGTAAACAGTA 81226
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Search completed: June 22, 2003, 08:44:00
Job time : 1921 secs

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: June 22, 2003, 08:03:44 ; Search time 236 Seconds
                                        171.763 Million cell updates/sec
                                        (without alignments)

Title: US-09-830-811-1
Perfect score: 18
Sequence: 18
              1 ggcggcttgtaaacagta 18

Scoring table: IDENTITY_NUC
Searched: Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Post-processing: Minimum Match 08
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters: 4370478

Database :   N_Geneseq_101002:*
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16.4	91.1	3489	22	AAF59534	cDNA encoding a mo
2	18	100.0	3914	15	AAQ44393	Sequence of human
3	18	100.0	3867	24	ABK35485	Human endometrial
4	18	100.0	3712	15	AAQ44392	Sequence of human
5	18	100.0	2625	22	AAF55586	Nucleotide sequenc
6	18	100.0	2625	20	AAV83124	Cadherin-11 cDNA.
7	18	100.0	2625	18	AAT61925	Full length human
8	18	100.0	2625	18	AAT85403	Human cadherin-11
9	18	100.0	2625	21	AAA53556	Human cadherin-11

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

c	10	16.4	91.1	3581	15	AAQ44391	Sequence of murine
c	11	16.4	91.1	4127	24	ABI99752	Mouse ischaemic co
c	12	15.4	85.6	302	20	AAV86757	EST clone AX309.
c	13	15.4	85.6	345	22	AAH53750	S. epidermidis ope
c	14	15.4	85.6	654	24	ABQ58717	S. epidermidis ope
c	15	15.4	85.6	808	22	AAH03710	Human colon cancer
c	16	15.4	85.6	880	22	AAK91670	Human cDNA clone (
c	17	15.4	85.6	880	22	AAK93833	Human cDNA 5'-end
c	18	15.4	85.6	1014	24	ABN90907	Staphylococcus epi
c	19	15.4	85.6	1206	24	AAH15306	Human cDNA clone r
c	20	15.4	85.6	1456	22	AAK94661	Human cDNA sequenc
c	21	15.4	85.6	2136	22	ABL60305	Human full-length
c	22	15.4	85.6	2307	19	AAV29267	Human bromo-functi
c	23	15.4	85.6	2713	22	AAI93435	Phosphatidylinosit
c	24	15.4	85.6	3268	22	AAH54030	S. epidermidis gen
c	25	15.4	85.6	7053	24	AAS26613	Human cDNA encodin
c	26	14.8	82.2	648	24	ABK78301	Bacillus clausii g
c	27	14.8	82.2	1350	24	ABN26266	Human ORFX polynuc
c	28	14.8	82.2	1466	24	ABA93939	Influenza A/udorn/
c	29	14.8	82.2	1606	21	AAC50109	Arabidopsis thalia
c	30	14.8	82.2	4873	22	AAC50109	Arabidopsis thalia
c	31	14.8	82.2	9373	22	AAC91400	Brassica napus BNM
c	32	14.8	82.2	12505	23	ABL07021	Arabidopsis thalia
c	33	14.8	80.0	60	24	ABL07020	Arabidopsis thalia
c	34	14.4	80.0	279	21	ABN36377	Human spliced tran
c	35	14.4	80.0	483	21	AAZ54273	Neisseria meningit
c	36	14.4	80.0	483	21	AAZ54272	Neisseria gonorrhe
c	37	14.4	80.0	483	21	AAZ54274	Neisseria meningit
c	38	14.4	80.0	825	21	AAC44203	Arabidopsis thalia
c	39	14.4	80.0	1177	21	AAA81778	N. meningitidis pa
c	40	14.4	80.0	1608	21	AAC41747	Arabidopsis thalia
c	41	14.4	80.0	2619	24	ABK83735	Human cDNA differe
c	42	14.4	1437668	349980	21	AAF21610	Neisseria meningit
c	43	14	77.8	297	24	AAA81490	N. meningitidis B
c	44	14	77.8	474	22	ABL87175	Human ovarian canc
c	45	14	77.8	652	22	AAH26610	Human P2Y-like GPC
		14	77.8			ABA13441	Human nervous syst

ALIGNMENTS

RESULT 1
AAA53556

ID   AAA53556 standard; DNA; 18 BP.
XX
AC   AAA53556;
XX
DT   22-NOV-2000 (first entry)
XX
DE   Human cadherin-11 antisense oligonucleotide OB-1.
XX
KW   Human; cadherin-11; cad-11; cell differentiation; pregnancy termination;
KW   carcinoma; antisense oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
PN   WO2002026236-A2.
XX
PD   11-MAY-2000.
XX
PF   29-OCT-1999; 99WO-CA01057.
XX
PR   30-OCT-1998; 98US-0106258.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   MacCalman CD;
XX
DR   WPI; 2000-365568/31.
XX
PT   Increasing or decreasing cad11 expression or function to modulate
PT   differentiation or neoplastic transformation of carcinoma cells to
PT   treat cancers -

XX
PS Claim 11; Page 22; 37pp; English.
XX
CC The present sequence is an antisense oligonucleotide for the human
CC cadherin-11 (cad-11) mRNA. It can be used to reduce the levels of cad-11
CC expression in cells, which is useful in the treatment of carcinomas,
CC particularly prostate tumour cells, for modulating the differentiation
CC of cells, and in the prevention or termination of pregnancy. It is
CC particularly useful for preventing metastasis of tumour cells.
XX
SQ Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 other;

Query Match   100.0%;   Score 18; DB 21; Length 18;
Best Local Similarity 100.0%;   Pred. No. 2;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 1 GGCGGCTTGTAAACAGTA 18
     ||||||||||||||||||
Db 1 GGCGGCTTGTAAACAGTA 18

RESULT 2
AAT85403/c
ID   AAT85403 standard; cDNA; 2625 BP.
XX
AC   AAT85403;
XX
DT   03-NOV-1997 (first entry)
XX
DE   Human cadherin-11 coding sequence.
XX
KW   Human; cadherin; rat; calcium-dependent cell adhesion protein;
KW   superfamily; cytoskeleton; eatenin; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   156.2546
FT   /*tag= a
FT   /product= Cadherin-11
XX
PN   US5646250-A.
XX
PD   08-JUL-1997.
XX
PF   17-APR-1992; 92US-0872643.
XX
PR   19-APR-1993; 93US-0049460.
PR   17-APR-1992; 92US-0872643.
PR   01-NOV-1994; 94US-0332638.
XX
PA   (DOHE-) DOHENY EYE INST.
XX
PI   Suzuki S;
XX
DR   WPI; 1997-362997/33.
XX
PT   Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion
XX
PS   Example 2; Column 87-90; 56pp; English.
XX
CC   This sequence encodes human cadherin-11. The invention specifically
CC   provides details of human cadherin-5, -8, -11 and rat
CC   cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell
CC   adhesion proteins. They are glycosylated integral membrane proteins
CC   that have an N-terminal extracellular domain that determines binding
CC   specificity, a hydrophobic membrane spanning region and a C-terminal
CC   cytoplasmic domain, which is highly conserved among members of the
CC   superfamily. The C-terminal domain interacts with the cytoskeleton
CC   through eatenins and other cytoskeleton-associated proteins. The
CC   novel cadherin proteins may be used in the analysis of the role of
CC   cadherins in various cancers. Sequence analysis of the cadherin
CC   proteins also allows investigation of the structure and function of
CC   cadherin. The cadherin proteins may be isolated by using anti-cadherin
CC   antibodies. These antibodies may also be used to modulate the activity
CC   of cadherin and to determine the tissue specific distribution of cadherin
CC   proteins. Each subclass of cadherins has a unique tissue distribution
CC   pattern.
XX
SQ   Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;

Query Match   100.0%;   Score 18; DB 18; Length 2625;
Best Local Similarity 100.0%;   Pred. No. 3,4;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGCGGCTTGTAAACAGTA 18
       ||||||||||||||||||
Db 185 GGCGGCTTGTAAACAGTA 168

RESULT 3
AAT61925/c
ID   AAT61925 standard; cDNA; 2625 BP.
XX
AC   AAT61925;
XX
DT   14-MAY-1997 (first entry)
XX
DE   Full length human cadherin-11 cDNA.
XX
KW   Ca2+ dependent; cell adhesion protein; foetal; cadherin; rat;
KW   brain; human; antibody; purification; determination;
KW   tissue expression; binding antagonist; calcium ion; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   156.2546
FT   /*tag= a
XX
PN   US5597725-A.
XX
PD   28-JAN-1997.
XX
PF   17-APR-1992; 92US-0872643.
XX
PR   26-JAN-1994; 94US-0188228.
PR   17-APR-1992; 92US-0872643.
PR   19-APR-1993; 93US-0049460.
XX
PA   (DOHE-) DOHENY EYE INST.
XX
PI   Suzuki S;
XX
DR   WPI; 1997-108328/10.
DR   P-PSDB; AAW13134.
XX
PT   Antibodies to cadherin proteins - useful as cadherin antagonists,
PT   etc.
XX
PS   Example 2; Columns 91-96; 59pp; English.
XX
CC   The present sequence encodes full length human cadherin-11, which
CC   is a Ca2+ dependent cell adhesion protein. The human cadherin cDNA
CC   was isolated from a foetal brain cDNA library, using probes based
CC   on homologous rat cadherin cDNA.
CC   Antibodies or fragments that specifically bind the human cadherin
CC   can be used to purify the cadherin, determine its tissue expression
CC   and antagonise its ligand/antiligand binding activities.
XX
SQ   Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;

Query Match   100.0%;   Score 18; DB 18; Length 2625;
Best Local Similarity 100.0%;   Pred. No. 3,4;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGCGGCTTGTAAAACAGTA 18
            ||||||||||||||||||||
Db   185 GGCGGCTTGTAAAACAGTA 168

RESULT 4
Db   AAV83124/c

ID   AAV83124 standard; cDNA; 2625 BP.
XX
AC   AAV83124;
XX
DT   02-MAR-1999 (first entry)
XX
DE   Cadherin-11 cDNA.
XX
KW   Cadherin; morphogenisis; calcium-dependent cell adhesion; pregnancy;
KW   endometrium; trophoblast; balstocyst; infertility; ss.
XX
OS   Homo sapiens.
XX
FH
FT   Key   Location/Qualifiers
FT
FT   CDS   155..2546
FT   /*tag= a
FT   /product= Cadherin-11
XX
PN   WO9849560-A1.
XX
PD   05-NOV-1998.
XX
PF   24-APR-1998;   98WO-CA00397.
XX
PR   25-APR-1997;   97CA-2203718.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Maclalman CD,   Stephenson MD;
XX
DR   WPI; 1999-024071/02.
DR   P-PSDB; AAW85598.
XX
PT   Assessing likelihood of successful pregnancy by measuring levels of
PT   cadherin-11 in endometrium - also diagnosis of infertility from low
PT   cadherin levels and increasing cadherin levels by administering
PT   progestin or cadherin-encoding DNA
XX
PS   Claim 7; Page 52-53; 63pp; English.
XX
CC   The likelihood of establishing and maintaining a pregnancy, blastocyst
CC   implantation or endometrial receptivity are determined by measuring the
CC   level of cadherin-11 mRNA or protein in endometrial cells. A level below
CC   a standard value indicates inability to establish or maintain pregnancy.
CC   Women who are identified as having low level expression of
CC   cadherin-11 in endometrial cells can then be treated with a genetic
CC   construct comprising the cadherin-11 cDNA. The expression of
CC   cadherin-11 from the construct increases fertility and lessens the
CC   likelihood of miscarriage. Cadherin-11 expression is a better predictor of
CC   cadherin-11 expression is a better predictor of endometrial response
CC   and receptiveness than conventional analysis of endometrial cell
CC   morphology.
XX
SQ   Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;

Query Match   100.0%; Score 18; DB 20; Length 2625;
Best Local Similarity   100.0%; Pred. No. 3.4;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGCGGCTTGTAAAACAGTA 18
            ||||||||||||||||||||
Db   185 GGCGGCTTGTAAAACAGTA 168

RESULT 5
Db   AAF55586/c

ID   AAF55586 standard; DNA; 2625 BP.
XX
AC   AAF55586;
XX
DT   29-MAY-2001 (first entry)
XX
DE   Nucleotide sequence of a human cadherin-11 polypeptide.
XX
KW   Human; cadherin-11; inflammatory joint disorder; chronic synovitis;
KW   autoimmune disorder; rheumatoid arthritis; arthritis; ss.
XX
OS   Homo sapiens.
XX
FH
FT   Key   Location/Qualifiers
FT
FT   CDS   156..2546
FT   /*tag= a
FT   /product= "cadherin-11"
XX
PN   WO200117557-A1.
XX
PD   15-MAR-2001.
XX
PF   01-SEP-2000;   2000WO-US24101.
XX
PR   03-SEP-1999;   99US-0152456.
PR   13-SEP-1999;   99US-0153490.
XX
PA   (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI   Brenner MB, Valencia X;
XX
DR   WPI; 2001-235163/24.
DR   P-PSDB; AAB67624.
XX
PT   Treating inflammatory joint disorders, e.g. chronic synovitis,
PT   autoimmune disorders and rheumatoid arthritis, comprises administering
PT   a cadherin-11 inhibitor that inhibits the binding of cadherin-11 to its
PT   counter receptor
XX
PS   Disclosure; Page 78-82; 89pp; English.
XX
CC   The present sequence encodes a human cadherin-11 polypeptide.
CC   Cadherin-11 is a transmembrane molecule that, inter alia, mediates
CC   binding of cells to each other through interaction with itself or its
CC   counter-receptors. Agents which inhibit cadherin-11, or which inhibit
CC   the binding of cadherin-11 to a cadherin-11 counter receptor are used
CC   to treat a subject having an inflammatory joint disorder. The method is
CC   useful for treating inflammatory joint disorders, e.g. chronic synovitis,
CC   autoimmune disorders, rheumatoid arthritis, lyme disease arthritis,
CC   arthritis associated with inflammatory bowel disease or with ankylosing
CC   spondylitis, Reiter's syndrome, or arthritis associated with systemic
CC   lupus erythematosus. The method may also be used for the rational drug
CC   design of new agents capable of modulating an immune system response.
CC   The nucleotide and amino acid sequences of cadherin-11 modulating agents
CC   may be used in computer-based modelling systems to predict the secondary
CC   and tertiary structure of the extracellular domain, and to target a
CC   toxin or a detectable agent to cells which express cadherin-11.
CC   counter-receptors or cadherin-11. The antibodies inhibiting the binding
CC   of cadherin-11 to its counter receptor may be used in screening assays
CC   for identifying pharmaceutical lead compounds in molecular libraries.
XX
SQ   Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;

Query Match   100.0%; Score 18; DB 22; Length 2625;
Best Local Similarity   100.0%; Pred. No. 3.4;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGCGGCTTGTAAAACAGTA 18
            ||||||||||||||||||||
Db   185 GGCGGCTTGTAAAACAGTA 168

RESULT 6
Db   AAF55586/c

AAQ44392/c
ID   AAQ44392 standard; cDNA to mRNA; 3712 BP.
XX
AC   AAQ44392;
XX
DT   14-SEP-1994 (first entry)
XX
DE   Sequence of human OSF-4-1 cDNA.
XX
OS   Homo sapiens.
XX
KW   OSF-4-1; cadherin; growth factor; osteogenesis; osteoblast; therapy;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   461..2851
FT   /*tag= a
XX
PN   EP585801-A.
XX
PD   09-MAR-1994.
XX
PF   25-AUG-1993; 93EP-0113602.
XX
PR   28-AUG-1992; 92JP-0230028.
XX
PT   New bone related, cadherin-like OSF-4 proteins - for treatment
PT   and diagnosis of bone metabolic disease, and nucleic acid
PT   encoding them
XX
PA   (FARH) HOECHST JAPAN LTD.
XX
PI   Amann E, Kawai S, Okazaki M, Takeshita S, Tsujimura A;
XX
PS   Claim 3; Page 18-22; 34pp; English.
XX
CC   cDNA libraries were constructed from the mouse osteoblastic cell
CC   line MC3T3-E1 and from mouse liver tissue, amplified by PCR, and
CC   then as much common DNA as possible removed by hybridisation between
CC   the 2 libraries. Residual E1-specific DNA was amplified, inserted
CC   into lambda gt10 and screened by plaque hybridisation. A minibank of
CC   273 E1-specific clones was recovered, their inserts amplified and
CC   used to screen total RNA from both cell types. One clone specific
CC   for E1 was identified and sequenced. The insert from this clone was
CC   used to screen cDNA prepd. from E1 RNA and the longest posn. insert
CC   cloned in pGEM 11zf (+) to give pKOT164. This insert was sequenced;
CC   it encoded the 796 AA mouse precursor protein (AAQ44391/R49730). The
CC   insert was also used to screen a cDNA bank prepd. from human
CC   osteosarcoma to identify 2 clones encoding the 2 human precursor
CC   proteins - OSF-4-1 and OSF-4-2 (AAQ44392/R49731 and AAQ44393/R49732
CC   respectively).
XX
SQ   Sequence 3712 BP; 1074 A; 856 C; 897 G; 885 T; 0 other;

Query Match   100.0%; Score 18; DB 15; Length 3712;
Best Local Similarity   100.0%; Pred. No. 3.5;
Matches   18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
            ||||||||||||||||||
Db   490 GGCGGCTTGTAAACAGTA 473

RESULT 7
ID   ABK35485 standard; DNA; 3867 BP.
XX
AC   ABK35485;
XX
DT   08-MAY-2002 (first entry)

XX
DE   Human endometrial cancer related gene, CDH11.
XX
KW   Human; ds; gene; endometrial cancer; differential expression;
KW   DNA microarray; protein microarray.
XX
OS   Homo sapiens.
XX
PN   WO20020209573-A2.
XX
PD   07-FEB-2002.
XX
PF   31-JUL-2001; 2001WO-US24104.
XX
PR   31-JUL-2000; 2000US-221735P.
XX
PA   (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI   Mutter GL;
XX
DR   WPI; 2002-179967/23.
DR   P-PSDB; AAU84265.
XX
PT   Diagnosing endometrial cancer comprises determining expression of
PT   nucleic acid molecules or expression products that are differentially
PT   expressed in normal and malignant endometrium -
XX
PS   Claim 1; Page 45-47; 233pp; English.
XX
CC   The invention relates to diagnosing endometrial cancer in a subject
CC   suspected of having endometrial cancer comprising determining the
CC   expression of a set of nucleic acid molecules or expression products in
CC   an endometrial sample suspected of being cancerous, where the set of
CC   nucleic acid molecules comprises at least 2 nucleic acid molecules
CC   selected from 50 fully defined sequences as given in the specification.
CC   The nucleic acids are used as an array of at least 2 of the 50
CC   nucleic acids bound to a solid substrate. Also included is a solid-phase
CC   protein microarray comprising at least 2 antibodies or its antigen
CC   binding fragments, that specifically bind at least 2 different
CC   polypeptides from the 50 fully defined sequences as given in the
CC   specification, fixed to a solid substrate. The methods and arrays are
CC   useful for the diagnosis of endometrial cancer, selecting and monitoring
CC   treatment regimes and identification of lead compounds useful for the
CC   treatment of endometrial cancer. The present sequence is one of 50
CC   genes differentially expressed between cancerous and non-cancerous
CC   samples.
XX
SQ   Sequence 3867 BP; 1098 A; 905 C; 932 G; 932 T; 0 other;

Query Match   100.0%; Score 18; DB 24; Length 3867;
Best Local Similarity   100.0%; Pred. No. 3.5;
Matches   18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
            ||||||||||||||||||
Db   506 GGCGGCTTGTAAACAGTA 489

RESULT 8
ID   AAQ44393 standard; cDNA to mRNA; 3914 BP.
XX
AC   AAQ44393;
XX
DT   14-SEP-1994 (first entry)
XX
DE   Sequence of human OSF-4-2 cDNA.
XX
KW   OSF-4-2; cadherin; growth factor; osteogenesis; osteoblast; therapy;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX

```
FH   Key             Location/Qualifiers
FT   CDS             491..2569
FT                   /*tag= a
XX
PN   EP585801-A.
XX
PD   09-MAR-1994.
XX
PF   25-AUG-1993; 93EP-0113602.
XX
PR   28-AUG-1992; 92JP-0230028.
XX
PA   (FARH ) HOECHST JAPAN LTD.
XX
PI   Amann E, Kawai S, Okazaki M, Takeshita S, Tsujimura A;
XX
PS   Claim 3; Page 23-27; 34pp; English.
XX
DR   WPI; 1994-076152/10.
DR   P-PSDB; AAR49732.
XX
PT   New bone related, cadherin-like OSF-4 proteins - for treatment
PT   and diagnosis of bone metabolic disease, and nucleic acid
PT   encoding them
XX
CC   cDNA libraries were constructed from the mouse osteoblastic cell
CC   line MC3T3-E1 and from mouse liver tissue, amplified by PCR, and
CC   then as much common DNA as possible removed by hybridisation between
CC   the 2 libraries. Residual E1-specific DNA was amplified, inserted
CC   into lambda gt10 and screened by plaque hybridisation. A minibank of
CC   273 E-specific clones was recovered, their inserts amplified and
CC   used to screen total RNA from both cell types. One clone specific
CC   for E1 was identified and sequenced. The insert from this clone was
CC   used to screen cDNA prepd. from E1 RNA and the longest posn. insert
CC   cloned in pGEM 112f (+) to give pKOT164. This insert was sequenced;
CC   it encoded the 796 AA mouse precursor protein (AAQ44391/R49730). The
CC   insert was also used to screen a cDNA bank prepd. from human
CC   osteosarcoma to identify 2 clones encoding the 2 human precursor
CC   proteins - OSF-4-1 and OSF-4-2 (AAQ44392/R49731 and AAQ44393/R49732
CC   respectively).
XX
SQ   Sequence 3914 BP; 1105 A; 920 C; 947 G; 942 T; 0 other;

Query Match             100.0%;  Score 18;  DB 15;  Length 3914;
Best Local Similarity   100.0%;  Pred. No. 3.5;
Matches    18;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1 GGCGGCGCTTGTAAACAGTA 18
            ||||||||||||||||||||
Db      520 GGCGGCGCTTGTAAACAGTA 503
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XX
PN   WO20010O235-A1.
XX
PD   04-JAN-2001.
XX
PF   29-JUN-2000; 2000WO-US17927.
XX
PR   29-JUN-1999; 99US-0342426.
XX
PA   (UYMC-) UNIV MCGILL.
PA   (CAPR-) CAPRION PHARM INC.
XX
PI   Cashman NR, Dodelet V, Paramithiotis E;
XX
PS   Disclosure; Page -; 77pp; English.
XX
DR   WPI; 2001-112393/12.
DR   P-PSDB; AAB59534.
XX
PT   Identifying prion protein binding proteins for use in diagnosis,
PT   treatment of prion-related diseases, neurodegenerative disorders, by
PT   detecting complex formation with detectable prion protein fusion
PT   protein -
XX
CC   The invention relates to a method of identifying a prion protein
CC   binding protein (PrPBP). The method comprises contacting a cell or
CC   biological sample with a detectable prion protein (PrP) fusion protein
CC   under conditions that allow complex formation between the fusion protein
CC   and a PrPBP, and detecting the complex, enabling the PrPBP to be
CC   identified. The invention also relates to a method for identifying a
CC   nucleic acid molecule which encodes PrPBP, which comprises providing a
CC   population of cells expressing a pool of nucleic acid molecules, where
CC   the cells do not normally express PrP on their cell surfaces; exposing
CC   the population of cells to detectably labelled PrP, and identifying a
CC   cell which binds the detectably labelled PrP, thereby enabling the
CC   nucleic acid encoding the PrPBP to be identified. The invention further
CC   relates to a method of detecting the abnormally folded pathogenic PrP
CC   isoform (PrP-Sc) in a sample using a PrPBP identified according to the
CC   invention; a method for screening potential inhibitors of PrP-Sc/PrPBP
CC   binding; the use of a PrPBP or PrP-binding portion thereof to inhibit
CC   PrP-Sc activity in a mammal or biological sample; the use of a PrPBP or
CC   PrP-binding portion thereof to treat a disorder associated with an
CC   undesirable level of interaction between the normally folded PrP-C and
CC   a PrPBP in a mammal; and a method of detecting B lymphocytes in a
CC   biological sample using a PrPBP. The invention also encompasses fusion
CC   proteins comprising PrP fused to alkaline phosphatase, or a PrPBP fused
CC   to alkaline phosphatase. PrPBPs, or the PrP-binding portions thereof, are
CC   useful for treating a disorder associated with PrP. The disorder may be
CC   a PrP-Sc-related disorder such as Creutzfeldt-Jakob disease (CJD), Kuru,
CC   fatal familial insomnia in humans, scrapie in sheep, and bovine
CC   spongiform encephalopathy (BSE) in cattle. The disorder may also be
CC   one associated with an undesirable level of interaction between the
CC   normally folded PrP-C and a PrPBP in a mammal such as cancer;
CC   neurodegenerative disorders, immunological disorders, abnormal
CC   proliferation or secretion of immunoglobulin, lymphoma, multiple
CC   myeloma, monoclonal gammopathy, B cell-related autoimmune diseases,
CC   myasthenia gravis, or rheumatoid arthritis. The present sequence
CC   represents cDNA encoding murine OB-cadherin-1. The present sequence
CC   as a moderate affinity PrPBP in the invention.
CC   Note: The present sequence is not shown in the specification, but
CC   was obtained from GenBank (accession number D21253).
XX
SQ   Sequence 3489 BP; 1053 A; 763 C; 791 G; 882 T; 0 other;

Query Match             91.1%;  Score 16.4;  DB 22;  Length 3489;
Best Local Similarity   94.4%;  Pred. No. 27;
Matches    17;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy        1 GGCGGGCTTGTAAACAGTA 18
            ||| ||||||||||||||||
Db      299 GGCGAGCTTGTAAACAGTA 282
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RESULT 9
AAF59534/c
ID   AAF59534 standard; cDNA; 3489 BP.
XX
AC   AAF59534;
XX
DT   24-APR-2001 (first entry)
XX
DE   cDNA encoding a mouse PrP-binding protein, OB-cadherin-1.
XX
KW   Mouse OB-cadherin-1; murine; prion protein binding protein; PrPBP;
KW   detectable Prp fusion protein; detection; diagnosis; B lymphocyte;
KW   PrP-Sc-associated disorder; prion disease; Creutzfeldt-Jakob disease;
KW   CJD; Kuru; fatal familial insomnia; scrapie; BSE;
KW   bovine spongiform encephalopathy; PrP-C-associated disorder;
KW   cancer; neurodegenerative disorder; immunological disorder;
KW   abnormal immunoglobulin secretion; lymphoma; multiple myeloma;
KW   monoclonal gammopathy; B cell-related autoimmune disease;
KW   myasthenia gravis; rheumatoid arthritis; ss.
XX
OS   Mus musculus.
```

```
RESULT 10
AAQ44391/c
ID   AAQ44391 standard; cDNA to mRNA; 3581 BP.
XX
AC   AAQ44391;
XX
DT   14-SEP-1994 (first entry)
XX
DE   Sequence of murine OSF-4 cDNA.
XX
KW   OSF-4; cadherin; growth factor; osteogenesis; osteoblast; therapy;
KW   diagnosis; ss.
XX
OS   Mus musculus.
XX
PN   EP585801-A.
XX
PD   09-MAR-1994.
XX
PF   25-AUG-1993; 93EP-0113602.
XX
PR   28-AUG-1992; 92JP-0230028.
XX
PA   (FARH ) HOECHST JAPAN LTD.
XX
PI   Amann E, Kawai S, Okazaki M, Takeshita S, Tsujimura A;
XX
DR   WPI; 1994-076152/10.
DR   P-PSDB; AAR49730.
XX
PT   New bone related, cadherin-like OSF-4 proteins - for treatment
PT   and diagnosis of bone metabolic disease, and nucleic acid
PT   encoding them
XX
PS   Claim 3; Page 13-17; 34pp; English.
XX
CC   cDNA libraries were constructed from the mouse osteoblastic cell
CC   line MC3T3-E1 and from mouse liver tissue, amplified by PCR, and
CC   then as much common DNA as possible removed by hybridisation.
CC   the 2 libraries. Residual E1-specific DNA was amplified, inserted
CC   into lambda gt10 and screened by plaque hybridisation. A minibank of
CC   273 E-specific clones was recovered, their inserts amplified and
CC   used to screen total RNA from both cell types. One clone specific
CC   for E1 was identified and sequenced. The insert from this clone was
CC   used to screen cDNA prepd. from E1 RNA and the longest posn. insert
CC   cloned in pGEM 11zf (+) to give pKOT164. This insert was sequenced;
CC   it encoded the 796 AA mouse precursor protein (AAQ44391/R49730). The
CC   insert was also used to screen a cDNA bank prepd. from human
CC   osteosarcoma to identify 2 clones encoding the 2 human precursor
CC   proteins - OSF-4-1 and OSF-4-2 (AAQ44392/R49731 and AAQ44393/R49732
CC   respectively).
XX
SQ   Sequence 3581 BP; 1121 A; 774 C; 800 G; 886 T; 0 other;

Query Match             91.1%;  Score 16.4;  DB 15;  Length 3581;
Best Local Similarity   94.4%;
Matches   17;  Conservative   0;  Mismatches  27;  Indels  0;  Gaps  0;

Qy           1 GGCGGCTTGTAAACAGTA 18
               |||||||||||||||||||
Db         313 GGCAGCTTGTAAACAGTA 296


RESULT 11
ABI99752/c
ID   ABI99752 standard; cDNA; 4127 BP.
XX
AC   ABI99752;
XX
```

(Left column)

```
XX
PN   WO9845435-A2.
XX
PD   15-OCT-1998.
XX
XX
PF   10-APR-1998;   98WO-US06954.
XX
PR   10-APR-1997;   97US-0835913.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ, Jacobs K,  Lavallie ER,  McCoy JM,  Merberg D;
PI   Racie LA, Spaulding V,  Treacy M;
XX
DR   WPI; 1999-070076/06.
XX
PT   New polynucleotides encoding human secreted proteins - derived from
PT   e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT   ovary, pituitary, retina and colon cDNA libraries
XX
PS   Claim 1; Page 339; 633pp; English.
XX
CC   This sequence represents an expressed sequence tag (EST), and is a
CC   polynucleotide of the invention. The polynucleotides of the invention are
CC   all secreted EST sequences isolated from a variety of human tissue
CC   sources. The EST sequences and proteins encoded by them are predicted to
CC   have useful biological activities which would make them suitable for
CC   treating, preventing or ameliorating medical conditions in humans and
CC   animals, although no supporting data is given. Suggested activities
CC   include nutritional activity, immune stimulating or suppressing activity,
CC   haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC   activity. The EST sequences are also stated to be useful for gene
CC   therapy.
XX
SQ   Sequence 302 BP; 44 A; 89 C; 56 G; 113 T; 0 other;

Qy   1 GGCGGCTTGTAAACAGT 17
        |||||||||||||||||
Db  81 GGCGGCTTGTGAAACAGT 65

Query Match      85.6%;  Score 15.4;  DB 20;  Length 302;
Best Local Similarity   94.1%;
Matches  16;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
                 Pred. No. 77;

RESULT 13
ID   AAH53750/c
     AAH53750 standard; DNA; 345 BP.
XX
AC   AAH53750;
XX
DT   03-SEP-2001 (first entry)
XX
DE   S. epidermidis open reading frame nucleotide sequence SEQ ID NO:2893.
XX
KW   Staphylococcus epidermidis SR1 strain; infection; diagnosis;.
KW   vaccination; endocarditis; ds.
XX
OS   Staphylococcus epidermidis.
XX
PN   WO20134809-A2.
XX
PD   17-MAY-2001.
XX
PF   09-NOV-2000;   2000WO-US30782.
XX
PR   09-NOV-1999;   99US-0164258.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
```

(Right column)

```
PI   Kimmerly WJ;
XX
DR   WPI; 2001-316495/33.
DR   P-PSDB; AAG82900.
XX
PT   Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT   useful for vaccinating against infections, e.g. endocarditis -
XX
     Claim 8; Page 754-755; 2188pp; English.
XX
CC   AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC   (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC   (I) and (II) can have antibacterial activity and therefore can be used
CC   in vaccination. The nucleic acids (I) may be used to produce the
CC   S. epidermidis polypeptides (II) via the production of vectors
CC   containing them which are used to produce hosts cells which express the
CC   polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC   used to vaccinate subjects and to raise antibodies against the bacteria.
CC   The polypeptides may also be used to assay for other inhibitors of their
CC   activity and therefore identify compounds that may be used for the
CC   treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC   AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC   polynucleotide sequences from the present invention. AAH55091 to
CC   AAH55098 represent oligonucleotide sequences and primers which are used
CC   in the exemplification of the present invention.
CC   N.B. The present invention specifically claims all the polynucleotide
CC   sequences given in the sequence listing of the present specification,
CC   however the sequence listing only goes up to SEQ ID NO:4454 so even
CC   though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,
CC   no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ   Sequence 345 BP; 115 A; 64 C; 67 G; 99 T; 0 other;

Qy   2 GCGGCTTGTAAACAGTA 18
        || ||||||||||||||
Db  23 GCAGCTTGTAAACAGTA 7

Query Match      85.6%;  Score 15.4;  DB 22;  Length 345;
Best Local Similarity   94.1%;
Matches  16;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
                 Pred. No. 78;

RESULT 14
ID   ABQ58777
     ABQ58777 standard; cDNA; 654 BP.
XX
AC   ABQ58777;
XX
DT   02-AUG-2002 (first entry)
XX
DE   Human colon cancer related nucleotide sequence SEQ ID NO:2472.
XX
KW   Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW   genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO20229086-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001;   2001WO-US30732.
XX
PR   02-OCT-2000;   2000US-2372271P.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Burgess C, Astle JH,  Carroll E,  Catino TJ,  Dwivedi P,  Molino GA;
PI   Thiaglingam A, Lewis ME;
XX
DR   WPI; 2002-426115/45.
XX
PT   New isolated nucleic acid that is differentially expressed in cancer
```

PT   tissues useful for determining the presence of colon cancer in a cell
PT   or tissue type, and in antisense therapy -
XX
PS   Claim 1; Fig 1; 796pp; English.
XX

CC   AB056306 to AB060787 represent isolated nucleic acids (I) differentially
CC   expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC   encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be
CC   used in antisense therapy. An antibody immunoreactive with a polypeptide
CC   encoded by (I) is useful for detecting cancer in a patient sample, and
CC   for detecting the presence or absence of a polynucleotide encoded by a
CC   nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC   from (I) can be used for determining the presence of a nucleic acid which
CC   hybridises to (I), and for determining the phenotype of cells in a sample
CC   of cells from a patient. (I) is useful for determining the presence of
CC   colon cancer in a cell or tissue type, for determining the presence or
CC   state of other type of cancer, in antisense therapy, to generate
CC   macroarrays on a solid surface, to identify a chromosome on which the
CC   corresponding gene resides, and in tissue profiling, forensics, genetic
CC   analysis, mapping and diagnostic applications. (I) can be used to raise
CC   antibodies, and to screen for peptide analogues and antagonists.
XX
SQ   Sequence 654 BP; 199 A; 122 C; 158 G; 168 T; 7 other;

Qy   1 GGCGGCTTGTAAACAGT 17
               |||||||||||||||||
Db   186 GGCGGCTTGTGAACAGT 202

RESULT 15
ID   AAH03710 standard; cDNA; 808 BP.
XX
AC   AAH03710;
XX
DT   26-JUN-2001 (first entry)
XX
DE   Human cDNA clone (5'-primer) SEQ ID NO:545.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
OS   Homo sapiens.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI   Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PR   28-JUL-2000; 2000EP-0116126.
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000;   2000JP-0118776.
PR   02-MAY-2000;   2000JP-0183767.
PR   09-JUN-2000;   2000JP-0241899.
XX

Primer sets for synthesizing polynucleotides, particularly the 5602
full-length cDNAs defined in the specification, and for the detection
and/or diagnosis of the abnormality of the proteins encoded by the
full-length cDNAs -

Claim 1; SEQ ID 545; 2537pp + CD ROM; English.

CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 808 BP; 265 A; 149 C; 200 G; 191 T; 3 other;

Qy   1 GGCGGCTTGTAAACAGT 17
               |||||||||||||||||
Db   123 GGCGGCTTGTGAACAGT 139

Search completed: June 22, 2003, 08:11:48
Job time : 240 secs

Query Match   85.6%; Score 15.4; DB 24; Length 654;
Best Local Similarity 94.1%; Pred. No. 83;
Matches 16; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Query Match   85.6%; Score 15.4; DB 22; Length 808;
Best Local Similarity 94.1%; Pred. No. 85;
Matches 16; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: June 22, 2003, 08:06:44 ; Search time 49 Seconds
(without alignments)
112.657 Million cell updates/sec

Title: US-09-830-811-1
Perfect score: 18
Sequence: 1 ggcggcttgtaaacagta 18

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :
       Issued_Patents_NA:*
  1: /cgn2_6/ptodata/1/1na/5A_COMB.seq:*
  2: /cgn2_6/ptodata/1/1na/5B_COMB.seq:*
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  5: /cgn2_6/ptodata/1/1na/PCTUS_COMB.seq:*
  6: /cgn2_6/ptodata/1/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	18	100.0	2625	1	US-08-188-228-57	Sequence 57, Appl
c 2	18	100.0	2625	1	US-08-332-643-51	Sequence 51, Appl
c 3	18	100.0	2625	1	US-08-332-638-57	Sequence 57, Appl
c 4	18	100.0	3712	1	US-08-738-349-3	Sequence 3, Appl
c 5	18	100.0	3914	2	US-08-738-349-5	Sequence 5, Appl
c 6	16.4	91.1	3581	2	US-08-738-349-1	Sequence 1, Appl
c 7	15.4	85.6	1014	2	US-09-134-001C-370	Sequence 370, App
c 8	15.4	85.6	2307	3	US-08-942-008-1	Sequence 1, Appl
c 9	14.8	82.2	38584	4	US-09-453-702B-50	Sequence 50, Appl
c 10·	13.8	76.7	336	2	US-08-606-293-3	Sequence 3, Appl
c 11	13.8	76.7	336	2	US-08-606-293-7	Sequence 7, Appl
c 12	13.8	76.7	1065	3	US-08-875-811-40	Sequence 40, Appl
c 13	13.8	76.7	1065	3	US-08-875-811-48	Sequence 48, Appl
c 14	13.8	76.7	1074	3	US-08-875-811-44	Sequence 44, Appl
c 15	13.8	76.7	1074	3	US-08-875-811-50	Sequence 50, Appl
c 16	13.8	76.7	1086	3	US-08-875-811-46	Sequence 46, Appl
c 17	13.8	76.7	1137	3	US-08-875-811-42	Sequence 42, Appl
c 18	13.8	76.7	1299	2	US-08-891-848-1	Sequence 1, Appl
c 19	13.8	76.7	1299	2	US-08-891-848-6	Sequence 6, Appl
c 20	13.8	76.7	1320	2	US-08-125-462-3	Sequence 3, Appl
c 21	13.8	76.7	1320	2	US-08-891-848-3	Sequence 3, Appl
c 22	13.8	76.7	2100	2	US-08-511-485-9	Sequence 9, Appl
c 23	13.8	76.7	2691	3	US-09-212-971-9	Sequence 9, Appl
c 24	13.8	76.7	2691	4	US-09-800-929A-9	Sequence 9, Appl
c 25	13.8	76.7	2691	2	US-09-617-053A-9	Sequence 9, Appl
c 26	13.8	76.7	6727	2	US-08-125-462-2	Sequence 2, Appl
c 27	13.8	76.7	6727	2	US-08-891-848-2	Sequence 2, Appl
c 28	13.8	76.7	6799	2	US-08-125-462-5	Sequence 5, Appl
c 29	13.8	76.7	6799	2	US-08-891-848-5	Sequence 5, Appl
c 30	13.8	76.7	6831	2	US-08-609-049A-27	Sequence 27, Appl
c 31	13.8	76.7	6831	4	US-09-170-996-27	Sequence 27, Appl
c 32	13.8	76.7	49136	4	US-09-422-869-1	Sequence 1, Appl
c 33	13.4	74.4	1197	5	PCT-US94-14277-7	Sequence 7, Appl
c 34	13.4	74.4	1566	4	US-08-871-572B-2	Sequence 2, Appl
c 35	13.4	74.4	2055	4	US-08-197-218-1	Sequence 1, Appl
c 36	13.4	74.4	2055	4	US-08-871-572B-3	Sequence 3, Appl
c 37	13.4	74.4	2791	4	US-09-571-367C-1	Sequence 1, Appl
c 38	13.4	74.4	3955	1	US-08-229-515A-14	Sequence 14, Appl
c 39	13.4	74.4	3955	2	US-08-645-865-14	Sequence 14, Appl
c 40	13.4	74.4	4566	2	US-08-465-976A-1	Sequence 1, Appl
c 41	13.4	74.4	4566	4	US-08-982-412-1	Sequence 1, Appl
c 42	13.4	74.4	50000	4	US-09-146-053-4	Sequence 4, Appl
c 43	13.2	73.3	173	1	US-08-435-684A-49	Sequence 49, Appl
c 44	13.2	73.3	173	4	US-08-934-877A-49	Sequence 49, Appl
c 45	13.2	73.3	173	4	US-08-871-678C-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-188-228-57/c
Sequence 57, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
  APPLICANT: Suzuki; Shintaro
  TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
  NUMBER OF SEQUENCES: 62
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
    ADDRESSEE: Borun
    STREET: 6300 Sears Tower, 233 S. Wacker Drive
    CITY: Chicago
    STATE: Illinois
    COUNTRY: USA
    ZIP: 60606
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/188,228
    FILING DATE:
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/049,460
    FILING DATE: 19 APR 1993
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/872,643
    FILING DATE: 17 APR 1992
  ATTORNEY/AGENT INFORMATION:
    NAME: NO. 5597725and, Greta E.
    REGISTRATION NUMBER: 35,302
    REFERENCE/DOCKET NUMBER: 31340
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (312) 474-6300
    TELEFAX: (312) 474-0448
    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 2625 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
US-08-188-228-57

Query Match   100.0%; Score 18; DB 1; Length 2625;
Best Local Similarity 100.0%; Pred. No. 0.56;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db  185 GGCGGCTTGTAAACAGTA 168
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RESULT 2
US-08-332-643-51/c
Sequence 51, Application US/0832643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 435
FILING DATE:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 2625 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-332-643-51

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Qy    1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db  185 GGCGGCTTGTAAACAGTA 168
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Query Match   100.0%; Score 18; DB 1; Length 2625;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-08-332-638-57/c
Sequence 57, Application US/0832638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 2625 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-332-638-57

```
Qy    1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db  185 GGCGGCTTGTAAACAGTA 168
```

Query Match   100.0%; Score 18; DB 1; Length 2625;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-08-738-349-3/c
Sequence 3, Application US/0873849
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349

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~  FILING DATE: 25-OCT-1996
~  CLASSIFICATION: 435
~  PRIOR APPLICATION DATA:
~    APPLICATION NUMBER: 435
~    FILING DATE:
~    APPLICATION NUMBER: US 08/364,439
~    FILING DATE: 26-AUG-1993
~    APPLICATION NUMBER: US 08/112,061
~    FILING DATE: 26-AUG-1993
~  ATTORNEY/AGENT INFORMATION:
~    NAME: Barker, M. P.
~    REGISTRATION NUMBER: 32,013
~    REFERENCE/DOCKET NUMBER: 02481.1323-00000
~    TELECOMMUNICATION INFORMATION:
~      TELEPHONE: 202-408-4000
~      TELEFAX: 202-408-4400
~ INFORMATION FOR SEQ ID NO: 3:
~   SEQUENCE CHARACTERISTICS:
~     LENGTH: 3712 base pairs
~     TYPE: nucleic acid
~     STRANDEDNESS: double
~     TOPOLOGY: linear
~   MOLECULE TYPE: cDNA to mRNA
~   ORIGINAL SOURCE:
~     ORGANISM: Homo sapiens
~     TISSUE TYPE: Osteosarcoma
~   FEATURE:
~     NAME/KEY: CDS
~     LOCATION: 461..2848
US-08-738-349-3

Query Match    100.0%;  Score 18;  DB 2;  Length 3712;
Best Local Similarity  100.0%;  Pred. No. 0.58;
Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 GGCGGCCTTGTAAACAGTA 18
          ||||||||||||||||||||
Db    490 GGCGGCCTTGTAAACAGTA 473

RESULT 5
US-08-738-349-5/c
Sequence 5, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
  APPLICANT: Takeshita, Sunao
  APPLICANT: Okazaki, Makoto
  APPLICANT: Kawai, Shinji
  APPLICANT: Tsujimura, Atsushi
  APPLICANT: Amann, Egon
  TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
  TITLE OF INVENTION: Process for Its Production
  NUMBER OF SEQUENCES: 12
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & .
    STREET: 1300 I Street, N.W.
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20005-3315
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/738,349
    FILING DATE: 25-OCT-1996
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/364,439
    FILING DATE:
    APPLICATION NUMBER: US 08/112,061
    FILING DATE: 26-AUG-1993
```

```
~  ATTORNEY/AGENT INFORMATION:
~    NAME: Barker, M. P.
~    REGISTRATION NUMBER: 32,013
~    REFERENCE/DOCKET NUMBER: 02481.1323-00000
~    TELECOMMUNICATION INFORMATION:
~      TELEPHONE: 202-408-4000
~      TELEFAX: 202-408-4400
~ INFORMATION FOR SEQ ID NO: 5:
~   SEQUENCE CHARACTERISTICS:
~     LENGTH: 3914 base pairs
~     TYPE: nucleic acid
~     STRANDEDNESS: double
~     TOPOLOGY: linear
~   MOLECULE TYPE: cDNA to mRNA
~   FEATURE:
~     NAME/KEY: CDS
~     LOCATION: 491..2569
US-08-738-349-5

Query Match    100.0%;  Score 18;  DB 2;  Length 3914;
Best Local Similarity  100.0%;  Pred. No. 0.58;
Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 GGCGGCCTTGTAAACAGTA 18
          ||||||||||||||||||||
Db    520 GGCGGCCTTGTAAACAGTA 503

RESULT 6
US-08-738-349-1/c
Sequence 1, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
  APPLICANT: Takeshita, Sunao
  APPLICANT: Okazaki, Makoto
  APPLICANT: Kawai, Shinji
  APPLICANT: Tsujimura, Atsushi
  APPLICANT: Amann, Egon
  TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
  TITLE OF INVENTION: Process for Its Production
  NUMBER OF SEQUENCES: 12
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & .
    STREET: 1300 I Street, N.W.
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20005-3315
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/738,349
    FILING DATE: 25-OCT-1996
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/364,439
    FILING DATE: 26-AUG-1993
    APPLICATION NUMBER: US 08/112,061
  ATTORNEY/AGENT INFORMATION:
    NAME: Barker, M. P.
    REGISTRATION NUMBER: 32,013
    REFERENCE/DOCKET NUMBER: 02481.1323-00000
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202-408-4000
      TELEFAX: 202-408-4400
~ INFORMATION FOR SEQ ID NO: 1:
~   SEQUENCE CHARACTERISTICS:
~     LENGTH: 3581 base pairs
```

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
STRAIN: osteoblastic cell line MC3T3E1
FEATURE:
NAME/KEY: CDS
LOCATION: 284..2671
US-08-738-349-1

Query Match
Best Local Similarity   91.1%;   94.4%;   Score 16.4; DB 2; Length 3581;
Matches 17; Conservative 0; Pred. No. 4.4; Mismatches 1; Indels 0; Gaps 0;

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Qy    1 GGCGGGCTTGTAAACAGTA 18
        | ||| |||||||||||
Db  313 GGCAGCTTGTAAACAGTA 296
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RESULT 7
US-09-134-001C-370/c
Sequence 370, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQUENCES: 5674
SEQ ID NO 370
LENGTH: 1014
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-370

Query Match
Best Local Similarity   85.6%;   94.1%;   Score 15.4; DB 4; Length 1014;
Matches 16; Conservative 0; Pred. No. 14; Mismatches 1; Indels 0; Gaps 0;

```
Qy    2 GCGGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db  692 GCAGCTTGTAAACAGTA 676
```

RESULT 8
US-08-942-008-1
Sequence 1, Application US/0894200B
Patent No. 6134419
GENERAL INFORMATION:
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: Nucleotide Sequences that Encode
TITLE OF INVENTION: Phosphatidylinositol-3' Kinase Associated Proteins and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: CA
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,008
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYX1027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 262-8710
TELEFAX: (510) 222-9758
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1928
US-08-942-008-1

Query Match
Best Local Similarity   85.6%;   94.1%;   Score 15.4; DB 3; Length 2307;
Matches 16; Conservative 0; Pred. No. 15; Mismatches 1; Indels 0; Gaps 0;

```
Qy     1 GGCGGGCTTGTAAACAGT 17
         ||||||||||||||||||
Db  1153 GGCGGGCTTGTAAACAGT 1169
```

RESULT 9
US-09-453-702B-50
Sequence 50, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: NO. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CURRENT APPLICATION DATA:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166

```
;   INFORMATION FOR SEQ ID NO: 50:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 38584
;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;     SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US-09-453-702B-50

Qy       1 GGCGGCCTTGTAAACAGTA 18
           |||||| || ||||||||||
Db   36134 GGCGGCCATGGAAACAGTA 36151

Query Match     82.2%;  Score 14.8;  DB 4;  Length 38584;
Best Local Similarity   88.9%;  Pred. No. 45;
Matches   16;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

RESULT 10
US-08-606-293-3
Sequence 3, Application US/0860293
Patent No. 5874082

;   GENERAL INFORMATION:
;     APPLICANT: de Boer, Mark
;     TITLE OF INVENTION: Humanized Anti-CD40 Monoclonal Antibodies and
;     TITLE OF INVENTION: Fragments Capable of Blocking B Cell Activation
;     NUMBER OF SEQUENCES: 8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: CHIRON CORPORATION Intellectual Property - R440
;       STREET: 4560 Horton Street, P.O. Box 8097
;       CITY: Emeryville
;       STATE: California
;       COUNTRY: United States of America
;       ZIP: 94662-8097
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: Patentin Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/606,293
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 424
;       CLASSIFICATION:
;       FILING DATE:
;     APPLICATION NUMBER: 08/070,158
;     FILING DATE: 28-MAY-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Savereide, Paul B.
;       REGISTRATION NUMBER: 36,914
;       REFERENCE/DOCKET NUMBER: 27527/33157
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (510) 601-2718
;       TELEFAX: (510) 655-3542
;       TELEX: n/a
;   INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 336 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: Protein
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 1..336

US-08-606-293-3

Query Match     76.7%;  Score 13.8;  DB 2;  Length 336;
Best Local Similarity   88.2%;  Pred. No. 92;
Matches   15;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy       2 GCGGCCTTGTAAACAGTA 18
           | ||||||||||||||||
```

```
Db      81 GAGCCTTGTAAACAGTA 97

RESULT 11
US-08-606-293-7
Sequence 7, Application US/0860293
Patent No. 5874082

;   GENERAL INFORMATION:
;     APPLICANT: de Boer, Mark
;     TITLE OF INVENTION: Humanized Anti-CD40 Monoclonal Antibodies and
;     TITLE OF INVENTION: Fragments Capable of Blocking B Cell Activation
;     NUMBER OF SEQUENCES: 8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: CHIRON CORPORATION Intellectual Property - R440
;       STREET: 4560 Horton Street, P.O. Box 8097
;       CITY: Emeryville
;       STATE: California
;       COUNTRY: United States of America
;       ZIP: 94662-8097
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: Patentin Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/606,293
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 424
;       FILING DATE: 28-MAY-1993
;       APPLICATION NUMBER: 08/070,158
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Savereide, Paul B.
;       REGISTRATION NUMBER: 36,914
;       REFERENCE/DOCKET NUMBER: 27527/33157
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (510) 601-2718
;       TELEFAX: (510) 655-3542
;       TELEX: n/a
;   INFORMATION FOR SEQ ID NO: 7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 336 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: Protein
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 1..336

US-08-606-293-7

Qy       2 GCGGCCTTGTAAACAGTA 18
           | ||||||||||||||||
Db      81 GAGCCTTGTAAACAGTA 97

Query Match     76.7%;  Score 13.8;  DB 2;  Length 336;
Best Local Similarity   88.2%;  Pred. No. 92;
Matches   15;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

RESULT 12
US-08-875-811-40/c
Sequence 40, Application US/08875811
Patent No. 6045793

;   GENERAL INFORMATION:
;     APPLICANT: Rybak, Susanna M.
;     APPLICANT: Newton, Dianne L.
;     APPLICANT: Boque, Lluis
;     APPLICANT: Wlodawer, Alexander
;     TITLE OF INVENTION: Recombinant Ribonuclease Proteins
;     NUMBER OF SEQUENCES: 64
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Townsend and Townsend and Crew LLP
```

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-24410OUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1065
OTHER INFORMATION: /note= "SFVFBMetGluOnc"
US-08-875-811-40

Query Match
Best Local Similarity   76.7%;   Score 13.8;   DB 3;
Matches   15;   Conservative   0;   Pred. No. 1.1e+02;   Length 1065;
                   Mismatches   2;   Indels   0;   Gaps   0;

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Qy    2  GCGGCTTGTAAACAGTA 18
         |||| |||||||||| ||||
Db  553  GCGGGTTGTAAATAGTA 537
```

RESULT 13
US-08-875-811-48/c
Sequence 48, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-24410OUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1065
OTHER INFORMATION: /note= "SFVOncMetSer"
US-08-875-811-48

Query Match
Best Local Similarity   76.7%;   Score 13.8;   DB 3;
Matches   15;   Conservative   0;   Pred. No. 1.1e+02;   Length 1065;
                   Mismatches   2;   Indels   0;   Gaps   0;

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Qy    2  GCGGCTTGTAAACAGTA 18
         |||| |||||||||| ||||
Db  553  GCGGGTTGTAAATAGTA 537
```

RESULT 14
US-08-875-811-44/c
Sequence 44, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.

REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-24410OUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1074
OTHER INFORMATION: /note= "MetSerOncA87FBE6"
US-08-875-811-44

Query Match   76.7%;   Score 13.8; DB 3; Length 1074;
Best Local Similarity 88.2%;   Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    2 GCGGCTTGTAAACAGTA 18
        |||| ||||||| ||||
Db  907 GCGGGTTGTAAATAGTA 891
```

RESULT 15
US-08-875-811-50/c
Sequence 50, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Parls, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-24410OUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1074
OTHER INFORMATION: /note= "MetGluOncFBE6"
US-08-875-811-50

Query Match   76.7%;   Score 13.8; DB 3; Length 1074;
Best Local Similarity 88.2%;   Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    2 GCGGCTTGTAAACAGTA 18
        |||| ||||||| ||||
Db  907 GCGGGTTGTAAATAGTA 891
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Search completed: June 22, 2003, 09:14:29
Job time : 51 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:44:05 ; Search time 142 seconds
(without alignments)
186.012 Million cell updates/sec

Title: US-09-830-811-1
Perfect score: 18
Sequence: 1 ggcggcttgtaaacagta 18
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Database :
Published_Applications_NA:*
  1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
  2: /cgn2_6/ptodata/2/pubpna/US07_PCT_NEW_PUB.seq:*
  3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
  4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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  7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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  9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	18	100.0	3403	12	US-10-044-090-597	Sequence 597, Appli
c 2	18	100.0	3867	10	US-09-919-497-5	Sequence 5, Appli
c 3	15.4	85.6	480	9	US-09-918-995-37236	Sequence 37236, A
c 4	15.4	85.6	7053	10	US-09-764-864-792	Sequence 792, App
c 5	14.8	82.2	142	10	US-09-878-574-9162	Sequence 9162, Ap
c 6	14.8	82.2	207	10	US-09-878-574-12381	Sequence 12381, A
c 7	14.8	82.2	222	10	US-09-878-574-12500	Sequence 12500, A
c 8	14.8	82.2	249	10	US-09-878-574-11388	Sequence 11388, A
c 9	14.8	82.2	473	9	US-09-918-995-10360	Sequence 10360, A
c 10	14.8	82.2	648	10	US-09-974-300-5592	Sequence 5592, Ap
c 11	14.8	82.2	1347	9	US-09-938-842A-208	Sequence 208, Appl
c 12	14.8	82.2	38584	9	US-10-114-170-50	Sequence 50, Appl
c 13	14.4	80.0	229	10	US-09-878-574-8610	Sequence 8610, Ap
c 14	14.4	80.0	383	9	US-09-918-995-6449	Sequence 6449, Ap
c 15	14.4	80.0	1069	10	US-09-833-381-1732	Sequence 1732, Ap
c 16	14.4	80.0	2804	9	US-10-198-846-10399	Sequence 10399, A
c 17	14.4	80.0	4084	12	US-10-044-090-221	Sequence 221, App
c 18	14	77.8	297	10	US-09-967-701-10153	Sequence 10153, A
c 19	14	77.8	312	10	US-09-923-876-3656	Sequence 3656, Ap
c 20	14	77.8	951	9	US-09-902-525-43	Sequence 43, Appl
c 21	14	77.8	1191	9	US-09-974-879-16	Sequence 16, Appl
c 22	14	77.8	1191	9	US-09-305-736-15	Sequence 15, Appl
c 23	14	77.8	1191	9	US-09-978-752-22	Sequence 22, Appl
c 24	14	77.8	465237	10	US-09-933-267A-1	Sequence 1, Appli
c 25	13.8	76.7	304	10	US-09-764-891-791	Sequence 791, Appl
c 26	13.8	76.7	339	10	US-09-978-752-7	Sequence 7, Appl1
c 27	13.8	76.7	340	10	US-09-910-943-623	Sequence 623, App
c 28	13.8	76.7	402	9	US-09-764-891-772	Sequence 772, App
c 29	13.8	76.7	437	10	US-09-764-891-6902	Sequence 6902, Ap
c 30	13.8	76.7	446	10	US-09-815-242-8488	Sequence 8488, Ap
c 31	13.8	76.7	723	10	US-09-815-242-4429	Sequence 4429, Ap
c 32	13.8	76.7	774	10	US-09-974-592-9	Sequence 9, Appl
c 33	13.8	76.7	879	10	US-09-201-936-40	Sequence 40, Appl
c 34	13.8	76.7	981	10	US-10-023-437-40	Sequence 40, Appl
c 35	13.8	76.7	984	10	US-09-764-891-8123	Sequence 8123, Ap
c 36	13.8	76.7	1827	9	US-08-781-986A-53	Sequence 53, Appl
c 37	13.8	76.7	2100	9	US-10-092-154-1315	Sequence 1315, Ap
c 38	13.8	76.7	2691	9	US-10-764-891-10139	Sequence 10139, A
c 39	13.8	76.7	5693	9	US-08-781-986A-53	Sequence 53, Appl
c 40	13.8	76.7	16592	9	US-10-092-154-1315	Sequence 1315, Ap
c 41	13.8	76.7	17849	9	US-09-764-891-10139	Sequence 10139, A
c 42	13.8	76.7	17849	9	US-10-092-154-1313	Sequence 1313, Ap
c 43	13.8	76.7	17862	9	US-09-764-891-10138	Sequence 10138, A
c 44	13.8	76.7	17862	9	US-09-764-847-1313	Sequence 1313, Ap
c 45	13.8	76.7	17862	10	US-09-764-847-1313	Sequence 1313, Ap

ALIGNMENTS

RESULT 1
US-10-044-090-597/c
Sequence 597, Application US/10044090
Patent No. US2002013708191

GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10,044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 597
LENGTH: 3403
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US2002013708191 1258943CB1

Query Match 100.0%; Score 18; DB 12; Length 3403;
Best Local Similarity 100.0%;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
         ||||||||||||||||||
Db 206 GGCGGCTTGTAAACAGTA 189

RESULT 2
US-09-919-497-5/c
Sequence 5, Application US/09919497
Patent No. US20020106662A1

GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31

; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.0
;
; SEQ ID NO 5
; LENGTH: 3867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-497-5

Qy
Query Match   100.0%;   Score 18;   DB 10;   Length 3867;
Best Local Similarity 100.0%;   Pred. No. 2.5;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGCGGCTTGTGAAACAGTA 18
          |||||||||||||||||||
Db   506 GGCGGCTTGTGAAACAGTA 489

RESULT 3
US-09-918-995-37236
; Sequence 37236, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37236
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(480)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37236

Query Match   85.6%;   Score 15.4;   DB 9;   Length 480;
Best Local Similarity   94.1%;   Pred. No. 53;
Matches   16; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 GGCGGCTTGTAAACAGT 17
          ||||||| |||||||||
Db   144 GGCGGCTTGTGAAACAGT 160

RESULT 4
US-09-764-864-792
; Sequence 792, Application US/09764864
; Patent No. US2002013275A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 792
; LENGTH: 7053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (154)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-792

Query Match   85.6%;   Score 15.4;   DB 10;   Length 7053;
Best Local Similarity   94.1%;   Pred. No. 79;
Matches   16; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 GGCGGCTTGTGAAACAGT 17
          |||||||||||||| |||
Db   1193 GGCGGCTTGTGAACAGT 1209

RESULT 5
US-09-878-574-9162/c
; Sequence 9162, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; SEQ ID NO 9162
; LENGTH: 142
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701102155H1
US-09-878-574-9162

Query Match   82.2%;   Score 14.8;   DB 10;   Length 142;
Best Local Similarity   88.9%;   Pred. No. 98;
Matches   16; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 GGCGGCTTGTAAACAGTA 18
          |||||||||||||||| |
Db   136 GGAGGCTTGTAAACAGGA 119

RESULT 6
US-09-878-574-12381/c
; Sequence 12381, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; SEQ ID NO 12381
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701065703H1
US-09-878-574-12381

Query Match   82.2%;   Score 14.8;   DB 10;   Length 207;
Best Local Similarity   88.9%;   Pred. No. 1e+02;
Matches   16; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 GGCGGCTTGTAAACAGTA 18
          || |||||||||||| |
Db   143 GGTGGCTTGTAAACAGGA 126

RESULT 7
US-09-878-574-12500/c
; Sequence 12500, Application US/0987857A
; Patent No. US20020105484A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 12500
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701065851H1
US-09-878-574-12500

```
Qy      1 GGCGGCTTGTAAACAGTA 18
          |||||||| ||||||||
Db    164 GGAGGCTTGTAAACAGGA 147
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Query Match   82.2%; Score 14.8; DB 10; Length 222;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches   16; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

RESULT 8
US-09-878-574-11388/c
; Sequence 11388, Application US/0987857A
; Patent No. US20020105484A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 11388
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701064387H1
US-09-878-574-11388

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Qy      1 GGCGGCTTGTAAACAGTA 18
          |||||||| ||||||||
Db    167 GGAGGCTTGTAAACAGGA 150
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Query Match   82.2%; Score 14.8; DB 10; Length 249;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches   16; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

RESULT 9
US-09-918-995-10360/c
; Sequence 10360, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10360
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(473)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-10360

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Qy      1 GGCGGCTTGTAAACAGTA 18
          |||||||| | ||||||
Db    377 GGCGGCTTCTAAACAGGA 360
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Query Match   82.2%; Score 14.8; DB 9; Length 473;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches   16; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

RESULT 10
US-09-974-300-5592
; Sequence 5592, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5592
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-5592

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Qy      1 GGCGGCTTGTAAACAGTA 18
          |||||||| |    |||
Db    536 GGCGGCTTGGAAAAAGTA 553
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Query Match   82.2%; Score 14.8; DB 10; Length 648;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches   16; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

RESULT 11
US-09-938-842A-208/c
; Sequence 208, Application US/09938842A
; Patent No. US20021603781A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24

RESULT 12
US-10-114-170-50
Sequence 50, Application US/10114170
Publication No. US20030023075A1
GENERAL INFORMATION:
  APPLICANT: Blattner, Frederick R.
              Burland, Valerie
              Perna, Nicole T.
              Plunkett, Guy
              Welch, Rod
  TITLE OF INVENTION:
  NUMBER OF SEQUENCES: 265
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Quarles & Brady
    STREET: 1 South Pinckney Street
    CITY: Madison
    STATE: WI
    COUNTRY: US
    ZIP: 53701-2113
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Word Perfect 8.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/114,170
    FILING DATE: 01-Apr-2002
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/453,702
    FILING DATE: 03-DEC-1999
    APPLICATION NUMBER: 60/110,955
    FILING DATE: 04-DEC-1998
  ATTORNEY/AGENT INFORMATION:
    NAME: Seay, Nicholas J.
    REGISTRATION NUMBER: 27386
    REFERENCE/DOCKET NUMBER: 960296.95017
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (608) 251-5000
    TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 50:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 38584
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Query Match   82.2%;   Score 14.8;   DB 9;   Length 38584;

US-10-114-170-50

Query Match   82.2%;   Score 14.8;   DB 9;   Length 1347;
Best Local Similarity   88.9%;   Pred. No. 1.4e+02;
Matches 16;   Conservative   0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy   1 GGCGGCCTTGTAAACAGTA 18
            | |||||||||||||| |
Db   1073 GGCGGCTTGTAAACCGGA 1056

SEQ ID NO 208
  LENGTH: 1347
  TYPE: DNA
  ORGANISM: Arabidopsis thaliana
US-09-938-842A-208

NUMBER OF SEQ ID NOS: 5379
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866

RESULT 13
US-09-878-574-8610/c
Sequence 8610, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
  APPLICANT: Byrum, Joseph R.
  APPLICANT: La Rosa, Thomas J.
  APPLICANT: Thompson, Michael D.
  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
  TITLE OF INVENTION: Plants
  FILE REFERENCE: 38-21(15401)B
  CURRENT APPLICATION NUMBER: US/09/878,574
  CURRENT FILING DATE: 2001-12-21
  PRIOR APPLICATION NUMBER: 09/333,535
  PRIOR FILING DATE: 1999-06-14
  NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 8610
  LENGTH: 229
  TYPE: DNA
  ORGANISM: Glycine max
  OTHER INFORMATION: Clone ID: 701101435H1
US-09-878-574-8610

Query Match   88.9%;   Score 14.8;   DB 9;   Length 229;
Best Local Similarity   88.9%;   Pred. No. 2.2e+02;
Matches 16;   Conservative   0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy   1 GGCGGCCTTGTAAACAGTA 18
            |||||| || |||||||||
Db   36134 GGCGGCCATGGAAACAGTA 36151

RESULT 14
US-09-918-995-6449/c
Sequence 6449, Application US/09918995
Publication No US20030073623A1
GENERAL INFORMATION:
  APPLICANT: Hyseq, Inc.
  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
  TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
  FILE REFERENCE: 20411-756
  CURRENT APPLICATION NUMBER: US/09/918,995
  CURRENT FILING DATE: 2001-07-30
  PRIOR APPLICATION NUMBER: US/09/235,076
  PRIOR FILING DATE: 1999-01-20
  NUMBER OF SEQ ID NOS: 38054
  SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6449
  LENGTH: 383
  TYPE: DNA
  ORGANISM: Homo sapiens
US-09-918-995-6449

Query Match   80.0%;   Score 14.4;   DB 10;   Length 383;
Best Local Similarity   93.8%;   Pred. No. 1.8e+02;
Matches 15;   Conservative   0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy   1 GGCGGCTTGTAAACAG 16
            || ||||||||||||||
Db   77 GGAGGCTTGTAAACAG 62

RESULT 15
US-09-833-381-1732/c
Sequence 1732, Application US/09833381

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; Patent No. US20020132090A1
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs
;  FILE REFERENCE: 5800-119
;  CURRENT APPLICATION NUMBER: US/09/833,381
;  CURRENT FILING DATE:  2001-04-11
;  PRIOR APPLICATION NUMBER: 09/516,448
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 2050
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1732
;  LENGTH: 1069
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(1069)
;  OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1732

Query Match        80.0%;  Score 14.4;  DB 10;  Length 1069;
Best Local Similarity   93.8%;  Pred. No. 2.2e+02;
Matches   15;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy.            1 GGCGGCTTGTAAACAG 16
                 |||||||||| |||
Db          1002 GGCGGCTTGTACACAG 987
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Run on: June 22, 2003, 08:07:40 ; Search time 2786 Seconds
                       (without alignments)
                       162.442 Million cell updates/sec

Title: US-09-830-811-1
Perfect score: 18
Sequence: 1 ggcggcttgtaaacagta 18

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Searched: 24791104 seqs, 12571243825 residues

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12: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
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26: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
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37: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
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41: /cgn2_6/ptodata/1/pna/US101B_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB ID	Description
1	18	100.0	18	32	US-09-830-811-1	Sequence 1, Appl1
2	18	100.0	377	25	US-09-644-871-4418	Sequence 4418, Ap
3	18	100.0	420	16	US-09-293-972-29969	Sequence 29969, A
4	18	100.0	420	34	US-09-904-939-29969	Sequence 29969, A
5	18	100.0	443	16	US-09-287-618-26653	Sequence 26653, A
6	18	100.0	492	31	US-09-824-518-5128	Sequence 5128, Ap
7	18	100.0	513	20	US-09-534-857-1848	Sequence 1848, Ap
8	18	100.0	619	25	US-09-644-871-7428	Sequence 7428, Ap
9	18	100.0	619	25	US-09-652-124-7882	Sequence 7882, Ap
10	18	100.0	2625	1	PCT-US02-18947-670	Sequence 670, App
11	18	100.0	2625	1	PCT-US93-03681-57	Sequence 57, Appl
12	18	100.0	2625	14	US-09-053-375B-1424	Sequence 1424, Ap
13	18	100.0	2625	18	US-09-403-441-1	Sequence 1, Appl
14	18	100.0	2625	18	US-09-442-589B-797	Sequence 797, App
15	18	100.0	2625	25	US-09-654-328-1	Sequence 1, Appl1
16	18	100.0	2625	41	US-10-172-118-670	Sequence 670, App
17	18	100.0	3296	50	US-10-163-818-1	Sequence 1, Appl1
18	18	100.0	3296	30	US-09-770-175-2189	Sequence 2189, Ap
19	18	100.0	3403	30	US-09-770-175-6393	Sequence 6393, Ap
20	18	100.0	3403	38	US-10-044-090-597	Sequence 597, App
21	18	100.0	3403	39	US-10-084-817-136	Sequence 136, App

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50: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
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83: /cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
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85: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*

c	22	18	100.0	3403	70	US-60-260-483-597	Sequence 597, App
c	23	18	100.0	3460	17	US-09-371-168-6588	Sequence 6588, App
c	24	18	100.0	3460	25	US-09-644-871-8016	Sequence 8016, Ap
c	25	18	100.0	3460	25	US-09-652-355-9125	Sequence 9125, Ap
c	26	18	100.0	3460	31	US-09-801-833-6588	Sequence 6588, Ap
c	27	18	100.0	3867	1	PCT-US01-24104-5	Sequence 5, Appli
c	28	18	100.0	3867	1	PCT-US01-24104A-5	Sequence 5, Appli
c	29	18	100.0	3867	1	PCT-US02-08456-485	Sequence 485, App
c	30	18	100.0	3867	34	US-09-919-497-5	Sequence 5, Appli
c	31	18	100.0	3867	76	US-60-324-185-30389	Sequence 30389, A
c	32	18	100.0	4022	25	US-09-644-871-9324	Sequence 9324, Ap
c	33	18	100.0	4022	26	US-09-667-547-1107	Sequence 1107, Ap
c	34	18	100.0	4022	26	US-09-698-012-1107	Sequence 1107, Ap
c	35	18	100.0	4022	27	US-09-698-014-8524	Sequence 8524, Ap
c	36	18	100.0	4022	28	US-09-716-285-5446	Sequence 5446, Ap
c	37	18	100.0	4022	28	US-09-710-990-1643	Sequence 1643, Ap
c	38	18	100.0	4022	29	US-09-721-588-5127	Sequence 5127, Ap
c	39	18	100.0	4022	29	US-09-726-174-5202	Sequence 5202, Ap
c	40	18	100.0	4022	29	US-09-726-789-4705	Sequence 4705, Ap
c	41	18	100.0	4022	29	US-09-726-808-5412	Sequence 5412, Ap
c	42	18	100.0	4022	29	US-60-213-360-3024	Sequence 3024, Ap
c	43	18	100.0	5232	65	US-60-213-360-4684	Sequence 4684, Ap
c	44	18	100.0	5232	65	US-60-278-258-9362	Sequence 9362, Ap
c	45	18	100.0	5232	71		

ALIGNMENTS

RESULT 1
US-09-830-811-1
Sequence 1, Application US/09830811
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: CADHERIN-11 EXPRESSION, AN ASSAY AND TREATMENT FOR CELLULAR INVASIVENESS
FILE REFERENCE: 80021-275
CURRENT APPLICATION NUMBER: US/09/830,811
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/106,258
PRIOR APPLICATION FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-830-811-1

Query Match   100.0%;   Score 18;   DB 32;   Length 18;
Best Local Similarity   100.0%;   Pred. No. 8.8;
Matches   18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy 1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db 1 GGCGGCTTGTAAACAGTA 18

RESULT 2
US-09-644-871-4418/c
Sequence 4418, Application US/09644871
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Pan, Yang
TITLE OF INVENTION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: THEREFOR
CURRENT APPLICATION NUMBER: 1600.1167-001
CURRENT FILING DATE: 1600.1167-001
PRIOR APPLICATION NUMBER: US/09/644,871
PRIOR APPLICATION FILING DATE: 2000-08-28
PRIOR APPLICATION FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 939
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4418
LENGTH: 377
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(377)
OTHER INFORMATION: n = A,T,C or G
US-09-644-871-4418

Query Match   100.0%;   Score 18;   DB 25;   Length 377;
Best Local Similarity   100.0%;   Pred. No. 15;
Matches   18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy 1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db 278 GGCGGCTTGTAAACAGTA 261

RESULT 3
US-09-293-972-29969/c
Sequence 29969, Application US/09293972
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-769
CURRENT APPLICATION NUMBER: US/09/293,972
CURRENT FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 34258
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29969
LENGTH: 420
TYPE: DNA
ORGANISM: Homo sapiens
US-09-293-972-29969

Query Match   100.0%;   Score 18;   DB 16;   Length 420;
Best Local Similarity   100.0%;   Pred. No. 15;
Matches   18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy 1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db 380 GGCGGCTTGTAAACAGTA 363

RESULT 4
US-09-904-939-29969/c
Sequence 29969, Application US/09904939
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-769
CURRENT APPLICATION NUMBER: US/09/904,939
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/293,972
PRIOR APPLICATION FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 34258
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29969
LENGTH: 420
TYPE: DNA
ORGANISM: Homo sapiens
US-09-904-939-29969

Query Match   100.0%;   Score 18;   DB 34;   Length 420;
Best Local Similarity   100.0%;   Pred. No. 15;
Matches   18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy 1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db 380 GGCGGCTTGTAAACAGTA 363

RESULT 5
US-09-287-618-26653/c
; Sequence 26653, Application US/09287618
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-768
; CURRENT APPLICATION NUMBER: US/09/287,618
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 35865
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26653
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(443)
; OTHER INFORMATION: n = A,T,C or G
US-09-287-618-26653

Query Match   100.0%;   Score 18;   DB 16;   Length 443;
Best Local Similarity 100.0%;   Pred. No. 15;
Matches   18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GGCGGCTTGTAAACAGTA 18
              ||||||||||||||||||
Db   427 GGCGGCTTGTAAACAGTA 410

RESULT 6
US-09-824-518-5128/c
; Sequence 5128, Application US/09824518
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2078-001
; CURRENT APPLICATION NUMBER: US/09/824,518
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/193,436
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10042
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5128
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-824-518-5128

Query Match   100.0%;   Score 18;   DB 31;   Length 492;
Best Local Similarity 100.0%;   Pred. No. 15;
Matches   18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GGCGGCTTGTAAACAGTA 18
              ||||||||||||||||||
Db   27 GGCGGCTTGTAAACAGTA 10

RESULT 7
US-09-534-857-1848/c
; Sequence 1848, Application US/09534857
; GENERAL INFORMATION:
; APPLICANT: Sellhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ADHESION PROTEINS AND L
; FILE REFERENCE: PD-1012 CIP
; CURRENT APPLICATION NUMBER: US/09/534,857
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 8920
; SOFTWARE: PERL Program
; SEQ ID NO 1848
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01314854
US-09-534-857-1848

Query Match   100.0%;   Score 18;   DB 20;   Length 513;
Best Local Similarity 100.0%;   Pred. No. 15;
Matches   18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GGCGGCTTGTAAACAGTA 18
              ||||||||||||||||||
Db   421 GGCGGCTTGTAAACAGTA 404

RESULT 8
US-09-644-871-7428/c
; Sequence 7428, Application US/09644871
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1167-001
; CURRENT APPLICATION NUMBER: US/09/644,871
; CURRENT FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: 60/151,059
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 9739
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7428
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-644-871-7428

Query Match   100.0%;   Score 18;   DB 25;   Length 619;
Best Local Similarity 100.0%;   Pred. No. 16;
Matches   18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GGCGGCTTGTAAACAGTA 18
              ||||||||||||||||||
Db   520 GGCGGCTTGTAAACAGTA 503

RESULT 9
US-09-652-124-7882/c
; Sequence 7882, Application US/09652124
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Welch, Nadine S.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1179-001
; CURRENT APPLICATION NUMBER: US/09/652,124
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,131
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 9868
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7882
; LENGTH: 619
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-652-124-7882

Qy Query Match   100.0%; Score 18; DB 25; Length 619;
    Best Local Similarity 100.0%; Pred. No. 16;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
         ||||||||||||||||||
Db 520 GGCGGCTTGTAAACAGTA 503

RESULT 10
PCT-US02-18947-670/c
; Sequence 670, Application PC/TUS0218947
; GENERAL INFORMATION:
; APPLICANT: Rosetta Inpharmatics
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-228
; CURRENT APPLICATION NUMBER: PCT/US02/18947
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 670
; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001797
; DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-670

Qy Query Match   100.0%; Score 18; DB 1; Length 2625;
    Best Local Similarity 100.0%; Pred. No. 20;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
         ||||||||||||||||||
Db 185 GGCGGCTTGTAAACAGTA 168

RESULT 11
PCT-US93-03681-57/c
; Sequence 57, Application PC/TUS9303681
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;   Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03681
; FILING DATE: 19930419
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2625 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US93-03681-57

Qy Query Match   100.0%; Score 18; DB 1; Length 2625;
    Best Local Similarity 100.0%; Pred. No. 20;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
         ||||||||||||||||||
Db 185 GGCGGCTTGTAAACAGTA 168

RESULT 12
US-09-053-375B-1424/c
; Sequence 1424, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvilli, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SEQ ID NO 1424
; LENGTH: 2625
; TYPE: DNA
; SOFTWARE: FastSEQ for Windows Version 4.0
; ORGANISM: Homo sapiens
US-09-053-375B-1424

Qy Query Match   100.0%; Score 18; DB 14; Length 2625;
    Best Local Similarity 100.0%; Pred. No. 20;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
         ||||||||||||||||||
Db 185 GGCGGCTTGTAAACAGTA 168

RESULT 13
US-09-403-441-1/c
; Sequence 1, Application US/09403441
; GENERAL INFORMATION:
; APPLICANT: MacCalman, Colin D
; APPLICANT: Stephenson, Mary D
; TITLE OF INVENTION: Cadherin-11 as an Indicator of Viable Pregnancy.
; FILE REFERENCE: 27866/34647
; CURRENT APPLICATION NUMBER: US/09/403,441
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/CA98/00397
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: CA 2,203,718
; PRIOR FILING DATE: 1997-04-25
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Homo sapiens
; SOFTWARE: PatentIn Ver. 2.0
US-09-403-441-1

Qy Query Match   100.0%; Score 18;
    Best Local Similarity 100.0%;

```
Matches    18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCGGGCTTGTAAACAGTA 18
          |||||||||||||||||||
Db    185 GGCGGGCTTGTAAACAGTA 168
```

```
RESULT 14
US-09-442-589B-797/c
; Sequence 797, Application US/09442589B
; GENERAL INFORMATION:
;   APPLICANT: Chenchik, Alex
;   APPLICANT: Lukashev, Matvey
;   TITLE OF INVENTION: Human Cardiovascular Array
;   FILE REFERENCE: CLON-006CIP10
;   CURRENT APPLICATION NUMBER: US/09/442,589B
;   CURRENT FILING DATE: 1999-11-17
;   PRIOR APPLICATION NUMBER: 09/053,375
;   PRIOR FILING DATE: 1998-03-31
;   NUMBER OF SEQ ID NOS: 1194
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 797
;   LENGTH: 2625
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-442-589B-797

Query Match             100.0%;  Score 18;  DB 18;  Length 2625;
Best Local Similarity   100.0%;  Pred. No. 20;
Matches    18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCGGGCTTGTAAACAGTA 18
          |||||||||||||||||||
Db    185 GGCGGGCTTGTAAACAGTA 168
```

```
RESULT 15
US-09-654-328-1/c
; Sequence 1, Application US/09654328
; GENERAL INFORMATION:
;   APPLICANT: Brenner, Michael B.
;   APPLICANT: Valencia, Xavier
;   TITLE OF INVENTION: Methods and Compositions for Treatment
;   TITLE OF INVENTION: of Inflammatory Disease Using Cadherin-11 Modulating Agents
;   FILE REFERENCE: B0801/7187/ERP/MAT
;   CURRENT APPLICATION NUMBER: US/09/654,328
;   CURRENT FILING DATE: 2000-09-01
;   PRIOR APPLICATION NUMBER: US 60/152,456
;   PRIOR FILING DATE: 1999-09-03
;   PRIOR APPLICATION NUMBER: US 60/153,490
;   PRIOR FILING DATE: 1999-09-13
;   NUMBER OF SEQ ID NOS: 12"
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 2625
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: (156)...(2546)
US-09-654-328-1

Query Match             100.0%;  Score 18;  DB 25;  Length 2625;
Best Local Similarity   100.0%;  Pred. No. 20;
Matches    18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGCGGGCTTGTAAACAGTA 18
          |||||||||||||||||||
Db    185 GGCGGGCTTGTAAACAGTA 168
```

Search completed: June 22, 2003, 10:01:12
Job time : 2790 secs

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: June 22, 2003, 08:11:55 ; Search time 774 Seconds
                 (without alignments)
                 161.805 Million cell updates/sec

Title: US-09-830-811-1
Perfect score: 18
Sequence: 1 ggcggcttgtaaacagta 18

Scoring table: IDENTITY.NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 7816976 seqs, 3478802793 residues

Total number of hits satisfying chosen parameters: 15633952

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Pending_Patents_NA_New:*
                 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
                 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
                 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
                 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
                 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
                 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2:*
                 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3:*
                 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
                 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
                 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3:*
                 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
                 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2:*
                 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	201	13	US-60-455-444-34244	Sequence 34244, A
2	18	100.0	201	13	US-60-455-444-34245	Sequence 34245, A
3	18	100.0	201	13	US-60-455-444-34246	Sequence 34246, A
4	18	100.0	201	13	US-60-455-444-34256	Sequence 34256, A
5	18	100.0	201	13	US-60-455-444-34257	Sequence 34257, A
6	18	100.0	201	13	US-60-455-444-34258	Sequence 34258, A
7	18	100.0	201	13	US-60-455-444-34268	Sequence 34268, A
8	18	100.0	201	13	US-60-455-444-34284	Sequence 34284, A
9	18	100.0	201	13	US-60-455-444-34286	Sequence 34286, A
10	18	100.0	201	13	US-60-455-241-34244	Sequence 34244, A
11	18	100.0	201	13	US-60-455-241-34245	Sequence 34245, A
12	18	100.0	201	13	US-60-455-241-34246	Sequence 34246, A
13	18	100.0	201	13	US-60-455-241-34256	Sequence 34256, A
14	18	100.0	201	13	US-60-455-241-34257	Sequence 34257, A
15	18	100.0	201	13	US-60-455-241-34258	Sequence 34258, A
16	18	100.0	201	13	US-60-455-241-34268	Sequence 34268, A
17	18	100.0	201	13	US-60-455-241-34284	Sequence 34284, A
18	18	100.0	201	13	US-60-455-241-34286	Sequence 34286, A
19	18	100.0	201	13	US-60-465-241-172763	Sequence 172763,
20	18	100.0	201	13	US-60-465-241-172766	Sequence 172766,
21	18	100.0	201	13	US-60-465-241-172912	Sequence 172912,
22	18	100.0	1026	6	US-09-724-676-6128	Sequence 6128, Ap
23	18	100.0	1026	6	US-09-724-676A-6128	Sequence 6128, Ap
24	18	100.0	2080	10	US-10-170-235-9735	Sequence 9735, Ap
25	18	100.0	2080	13	US-60-455-241-2624	Sequence 2624, Ap
26	18	100.0	2080	13	US-60-455-241-2624	Sequence 2624, Ap
27	18	100.0	2625	9	US-10-34?-887-670	Sequence 670, Appl
28	18	100.0	2625	10	US-10-269-909-6	Sequence 6, Appl
29	18	100.0	3210	6	US-09-724-676-6129	Sequence 6129, Ap
30	18	100.0	3210	6	US-09-724-676A-6129	Sequence 6129, Ap
31	18	100.0	3661	8	PCT-US03-15711-151	Sequence 151, App
32	18	100.0	3661	8	PCT-US03-15711-151	Sequence 151, App
33	18	100.0	3691	10	US-10-440-464-151	Sequence 151, App
34	18	100.0	3691	10	US-10-241-425-9237	Sequence 9237, Ap
35	18	100.0	3691	9	US-10-170-235-9237	Sequence 9237, Ap
36	18	100.0	3691	13	US-60-455-241-2623	Sequence 2623, Ap
37	18	100.0	3691	13	US-60-455-241-2623	Sequence 2623, Ap
38	18	100.0	3867	1	PCT-US02-14597-22	Sequence 22, Appl
39	18	100.0	3867	8	PCT-US03-15711-152	Sequence 152, App
40	18	100.0	3867	8	PCT-US03-15711-152	Sequence 152, App
41	18	100.0	3867	10	US-10-444-464-152	Sequence 152, App
42	18	100.0	3867	10	US-10-240-425-1211	Sequence 1211, App
43	18	100.0	6536	9	US-10-101-510-485	Sequence 485, APP
44	18	100.0	6536	10	US-10-170-235-10098	Sequence 10098, A
45	18	100.0	6536	13	US-60-455-444-2625	Sequence 2625, Ap
			6536	13	US-60-455-444-2625	Sequence 2625, Ap
			122184	13	US-60-465-241-52470	Sequence 52470, A

ALIGNMENTS

RESULT 1
US-60-455-444-34244/c
Sequence 34244, Application US/60455444

GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele
  APPLICANT: BEGOVICH, Ann
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
  TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001455
  CURRENT APPLICATION NUMBER: US/60/455,444
  CURRENT FILING DATE: 2003-03-18
  NUMBER OF SEQ ID NOS: 50986
  SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 34244
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
US-60-455-444-34244

Query Match   100.0%; Score 18; DB 13; Length 201;
Best Local Similarity   100.0%; Pred. No. 6.1;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGCGGCTTGTAAACAGTA 18
              ||||||||||||||||||
Db   44 GGCGGCTTGTAAACAGTA 27

RESULT 2
US-60-455-444-34245/c
Sequence 34245, Application US/60455444

GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele
  APPLICANT: BEGOVICH, Ann
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
  TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001455
  CURRENT APPLICATION NUMBER: US/60/455,444
  CURRENT FILING DATE: 2003-03-18
  NUMBER OF SEQ ID NOS: 50986
  SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 34245
  LENGTH: 201

; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-455-444-34245

Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db   37 GGCGGCTTGTAAACAGTA 20

RESULT 3
US-60-455-444-34246/c
; Sequence 34246, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34246
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-455-444-34246

Query Match   100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches   18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db   32 GGCGGCTTGTAAACAGTA 15

RESULT 4
US-60-455-444-34256/c
; Sequence 34256, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34256
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-455-444-34256

Query Match   100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches   18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db   44 GGCGGCTTGTAAACAGTA 27

RESULT 5
US-60-455-444-34257/c
; Sequence 34257, Application US/60455444
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34257
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-455-444-34257

Query Match   100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches   18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db   37 GGCGGCTTGTAAACAGTA 20

RESULT 6
US-60-455-444-34258/c
; Sequence 34258, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34258
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-455-444-34258

Query Match   100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches   18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db   32 GGCGGCTTGTAAACAGTA 15

RESULT 7
US-60-455-444-34268/c
; Sequence 34268, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34268
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-455-444-34268

Query Match   100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db  32 GGCGGCTTGTAAACAGTA 15
```

RESULT 8
US-60-455-444-34284/c
Sequence 34284, Application US/60455444
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001455
CURRENT APPLICATION NUMBER: US/60/455,444
CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34284
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-455-444-34284

Query Match 100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db  44 GGCGGCTTGTAAACAGTA 27
```

RESULT 9
US-60-455-444-34286/c
Sequence 34286, Application US/60455444
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001455
CURRENT APPLICATION NUMBER: US/60/455,444
CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34286
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-455-444-34286

Query Match 100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db  37 GGCGGCTTGTAAACAGTA 20
```

RESULT 10
US-60-465-241-34244/c
Sequence 34244, Application US/60465241
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001468
CURRENT APPLICATION NUMBER: US/60/465,241

CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34244
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-465-241-34244

Query Match 100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db  44 GGCGGCTTGTAAACAGTA 27
```

RESULT 11
US-60-465-241-34245/c
Sequence 34245, Application US/60465241
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001468
CURRENT APPLICATION NUMBER: US/60/465,241
CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34245
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-465-241-34245

Query Match 100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db  37 GGCGGCTTGTAAACAGTA 20
```

RESULT 12
US-60-465-241-34246/c
Sequence 34246, Application US/60465241
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001468
CURRENT APPLICATION NUMBER: US/60/465,241
CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34246
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-465-241-34246

Query Match 100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 GGCGGCTTGTAAACAGTA 18
        ||||||||||||||||||
Db  32 GGCGGCTTGTAAACAGTA 15
```

RESULT 13
US-60-465-241-34256/c
Sequence 34256, Application US/60465241
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001468
CURRENT APPLICATION NUMBER: US/60/465,241
CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34256
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-465-241-34256

Query Match   100.0%; Score 18; DB 13; Length 201;
Best Local Similarity   100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTGTAAACAGTA 18
        ||||||||||||||||||||
Db   44 GGCGGCTTGTGTAAACAGTA 27

RESULT 14
US-60-465-241-34257/c
Sequence 34257, Application US/60465241
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001468
CURRENT APPLICATION NUMBER: US/60/465,241
CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34257
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-465-241-34257

Query Match   100.0%; Score 18; DB 13; Length 201;
Best Local Similarity   100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTGTAAACAGTA 18
        ||||||||||||||||||||
Db   37 GGCGGCTTGTGTAAACAGTA 20

RESULT 15
US-60-465-241-34258/c
Sequence 34258, Application US/60465241
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001468
CURRENT APPLICATION NUMBER: US/60/465,241
CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34258
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-465-241-34258

Query Match   100.0%; Score 18; DB 13; Length 201;
Best Local Similarity   100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTGTAAACAGTA 18
        ||||||||||||||||||||
Db   32 GGCGGCTTGTGTAAACAGTA 15

Search completed: June 22, 2003, 10:14:19
Job time : 776 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: June 22, 2003, 08:06:05 ; Search time 1754 Seconds
                                           (without alignments)
                                           166.202 Million cell updates/sec

Title: US-09-830-811-1
Perfect score: 18
Sequence: 1 ggcggcttgtaaacagta 18
Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   EST:*
                 1: em_estba:*
                 2: em_esthum:*
                 3: em_estin:*
                 4: em_estmu:*
                 5: em_estov:*
                 6: em_estpl:*
                 7: em_estro:*
                 8: em_htc:*
                 9: em_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: gb_gss:*
                 18: gb_gss:*
                 19: em_gss_hum:*
                 20: em_gss_inv:*
                 21: em_gss_pln:*
                 22: em_gss_vrt:*
                 23: em_gss_fun:*
                 24: em_gss_mam:*
                 25: em_gss_mus:*
                 26: em_gss_other:*
                 27: em_gss_pro:*
                 27: em_gss_rod:*

SUMMARIES

Result   %   Query
No.   Score   Match Length DB   ID   Description
----- -----   ----- ------ --- --   -----------
c   1   18'   100.0   579   9   AL708659   AL708659 DKFZp686K
c   2   18   100.0   585   12   BF194811   BF194811 7o93h03.x
c   3   18   100.0   943   9   AU133055   AU133055 AU133055
c   4   18   100.0   960   9   AU132966   AU132966 AU132966
c   5   18   100.0   964   12   BF337900   BF337900 602035724
c   6   17   94.4   239   9   AA091280   AA091280 cchn2408.

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

No.										
c 7	16.4	91.1	384	10	AW125499		AW125499 UI-M-BH2.
c 8	16.4	91.1	451	9	AI465790		AI465790 vw97g05.y
c 9	16.4	91.1	453	12	BG802493		BG802493 0l8l-71 M
c 10	16.4	91.1	455	10	BB854489		BB854489 2091-94 M
c 11	16.4	91.1	479	10	BB854982		BB854982
c 12	16.4	91.1	498	9	AI391334		AI391334 mb72g07.y
c 13	16.4	91.1	501	10	AA839644		AA839644 vw97g05.r
c 14	16.4	91.1	509	14	BM934786		BM934786 UI-M-BH2.
c 15	16.4	91.1	539	12	BF464496		BF464496 UI-M-CG0p
c 16	16.4	91.1	566	10	AW586982		AW586982 EST318605
c 17	16.4	91.1	569	9	AI118833		AI118833 uc14c12.r
c 18	16.4	91.1	569	10	BB650583		BB650583
c 19	16.4	91.1	600	12	BG800007		BG800007
c 20	16.4	91.1	600	12	BG808443		BG808443
c 21	16.4	91.1	601	10	BB652650		BB652650
c 22	16.4	91.1	620	10	AW822684		AW822684 ug17a02.y
c 23	16.4	91.1	623	10	BB619131		BB619131
c 24	16.4	91.1	642	10	BB660181		BB660181
c 25	16.4	91.1	645	10	BB656306		BB656306
c 26	16.4	91.1	650	10	AW210019		AW210019 u150a04.y
c 27	16.4	91.1	656	10	BB627470		BB627470 BB627470
c 28	16.4	91.1	656	10	BI558800		BI558800 603241032
c 29	16.4	91.1	659	10	BB622135		BB622135 BB622135
c 30	16.4	91.1	681	10	AW209556		AW209556 u144d05.y
c 31	16.4	91.1	681	10	BB642928		BB642928 BB642928
c 32	16.4	91.1	689	10	BB198426		BB198426 ug78d12.y
c 33	16.4	91.1	706	10	BB198551		BB198551 ug79h05.y
c 34	16.4	91.1	760	10	BH726531		BH726531 BOMOI40YR
c 35	16.4	91.1	776	13	BI734469		BI734469 603353919
c 36	16.4	91.1	797	10	BF234442		BF234442 602028235
c 37	16.4	91.1	801	9	AU080267		AU080267 AU080267
c 38	16.4	91.1	834	13	BI689448		BI689448 603315308
c 39	16.4	91.1	844	14	BQ143991		BQ143991 NF018A11D
c 40	16.4	91.1	907	14	BQ891796		BQ891796 AGENCOURT
c 41	16.4	91.1	926	12	BF179053		BF179053 60l80678l
c 42	16.4	91.1	952	10	AK012880		AK012880 Mus muscu
c 43	16.4	91.1	970	14	BQ712732		BQ712732 AGENCOURT
c 44	16.4	91.1	1159	14	BQ930532		BQ930532 AGENCOURT
c 45	16.4	91.1	1308	11	AK009182		AK009182 Mus muscu

ALIGNMENTS

RESULT 1
AL708659/c
LOCUS   AL708659   579 bp   mRNA   linear   EST 22-MAR-2002
DEFINITION DKFZp686K1153_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686K1153 5', mRNA sequence.
ACCESSION   AL708659
VERSION   AL708659.1 GI:19692014
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 579)
  AUTHORS   Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
  TITLE   EST (Wambutt,R.; Heubner,D.; Mewes,H.W.; Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Wambutt R
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686K1153) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES   Location/Qualifiers

```
source          1. .579
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="DKFZp686K1153"
                /clone_lib="686 (synonym: hlcc3)"
                /tissue_type="human skeletal muscle"
                /dev_stage="adult"
                /lab_host="DH10B"
                /note="Vector:pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                cDNA-collection:"

BASE COUNT     122 a     158 c     191 g     107 t     1 others
ORIGIN

Qy       1 GGCGGGCTTGTAAACAGTA 18
           ||||||||||||||||||
Db     468 GGCGGGCTTGTAAACAGTA 451

RESULT 2
LOCUS       BF194811      585 bp    mRNA    linear   EST 03-NOV-2000
DEFINITION  7o93h03.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644020 3'
            similar to TR:Q15066 Q15066 OB-CADHERIN-2. ;, mRNA sequence.
ACCESSION   BF194811
VERSION     BF194811.1  GI:11080564
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
            Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            High quality sequence stop: 508.

FEATURES             Location/Qualifiers
     source          1. .585
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3644020"
                     /clone_lib="NCI_CGAP_Ov18"
                     /tissue_type="fibrotheoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGACGCGGCCGCACAATTTTTTTTTTTTTTTTT 3'];
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT     118 a     167 c     193 g     107 t
ORIGIN

Qy       1 GGCGGGCTTGTAAACAGTA 18
           ||||||||||||||||||
Db     509 GGCGGGCTTGTAAACAGTA 492
```

```
Qy   1. .579
     /organism="Homo sapiens"

Query Match     100.0%;  Score 18;  DB 9;  Length 579;
Best Local Similarity   100.0%;  Pred. No. 29;
Matches   18;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1 GGCGGGCTTGTAAACAGTA 18
           ||||||||||||||||||
Db     468 GGCGGGCTTGTAAACAGTA 451
```

```
Qy       1 GGCGGGCTTGTAAACAGTA 18
           ||||||||||||||||||
Db     504 GGCGGGCTTGTAAACAGTA 487

RESULT 3
LOCUS       AU133055      943 bp    mRNA    linear   EST 01-AUG-2002
DEFINITION  AU133055 NT2RP4 Homo sapiens cDNA clone NT2RP4001171 5', mRNA
            sequence.
ACCESSION   AU133055
VERSION     AU133055.1  GI:10993594
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 943)
  AUTHORS   Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
            Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
            Isogai,T.
  TITLE     HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
            Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano
            ,S., Masuho,Y., Isogai,T.)
  JOURNAL   Unpublished (2000).
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.

FEATURES             Location/Qualifiers
     source          1. .943
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="NT2RP4001171"
                     /clone_lib="NT2RP4"
                     /cell_type="teratocarcinoma"
                     /cell_line="NT2"
                     /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
                     cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT     211 a     250 c     295 g     182 t     5 others
ORIGIN

Qy       1 GGCGGGCTTGTAAACAGTA 18
           ||||||||||||||||||||
Db     250 GGCGGGCTTGTAAACAGTA 182
```

```
Query Match     100.0%;  Score 18;  DB 9;  Length 943;
Best Local Similarity   100.0%;  Pred. No. 35;
Matches   18;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1 GGCGGGCTTGTAAACAGTA 18
           ||||||||||||||||||||
Db     509 GGCGGGCTTGTAAACAGTA 492

RESULT 4
LOCUS       AU132966      960 bp    mRNA    linear   EST 01-AUG-2002
DEFINITION  AU132966 NT2RP4 Homo sapiens cDNA clone NT2RP4000986 5', mRNA
            sequence.
ACCESSION   AU132966
VERSION     AU132966.1  GI:10993505
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 960)
  AUTHORS   Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
```

TITLE   HRI human cDNA project (Ota,T., Sugiyama,T., Nishikawa,T., Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano
AUTHORS   Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
          Isogai,T.
          ,S., Masuho,Y., Isogai,T.)
          Unpublished (2000)
COMMENT   Contact: Takao Isogai
          Genomics Laboratory
          Helix Research Institute
          1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: genomics@hri.co.jp
          HRI human cDNA project; cDNA library construction: Department of
          Research Institute; cDNA library construction: Helix
          Virology, Institute of Medical Science, University of Tokyo, and
          Helix Research Institute.
FEATURES   Location/Qualifiers
     source   1..960
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="NT2RP4000986"
                     /clone_lib="NT2RP4"
                     /cell_type="teratocarcinoma"
                     /cell_line="NT2"
                     /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
                     cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT   222 a   249 c   292 g   190 t   7 others
ORIGIN
Qy   1 GGCGGGCTTGTAAACAGTA 18
             ||||||||||||||||||
Db   467 GGCGGGCTTGTAAACAGTA 450

Query Match   100.0%; Score 18; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 35;
Matches   18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
BF337900/c
LOCUS   BF337900   964 bp   mRNA   linear   EST 22-NOV-2000
DEFINITION 602035724F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183901
            5', mRNA sequence.
ACCESSION   BF337900
VERSION   BF337900.1 GI:11284275
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 964)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9500 row: o column: 06
            High quality sequence stop: 672.
FEATURES   Location/Qualifiers
     source   1..964
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4183901"
                     /clone_lib="NCI_CGAP_Brn64"
                     /tissue_type="glioblastoma, with EGFR amplification"

TITLE   /lab_host="DH10B (T1 phage-resistant)"
            /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.57 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT   259 a   252 c   295 g   158 t
ORIGIN
Qy   1 GGCGGGCTTGTAAACAGTA 18
             ||||||||||||||||||
Db   206 GGCGGGCTTGTAAACAGTA 189

Query Match   100.0%; Score 18; DB 12; Length 964;
Best Local Similarity 100.0%; Pred. No. 35;
Matches   18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
AA091280
LOCUS   AA091280   239 bp   mRNA   linear   EST 24-OCT-1996
DEFINITION cchn2408.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
            cDNA 5', mRNA sequence.
ACCESSION   AA091280
VERSION   AA091280.1 GI:1635864
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 239)
AUTHORS   Liew,C.C.
TITLE   cDNAs from fetal heart (1996)
JOURNAL   Unpublished (1996)
COMMENT   Contact: Liew CC
            Brigham and Women's Hospital
            Harvard Medical School
            75 Francis St. Boston, MA 02115, USA
            Tel: 617328915
            Fax: 617750995
            Email: cliew@rics.bwh.harvard.edu
            PCR Primers
            FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
            BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
            Seq primer: 5' GAAATTAACCCTCACTAAAGG 3'.
FEATURES   Location/Qualifiers
     source   1..239
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human fetal heart, Lambda ZAP Express"
                     /lab_host="E. coli XL1-Blue"
                     /note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
                     XhoI; mRNA was purified from human fetal hearts (8-10
                     weeks). cDNA was synthesized using a XhoI-Oligo dT
                     adaptor-primer. EcoRI adaptors were ligated, followed by
                     digestion with XhoI for directional cloning into
                     predigested lambda ZAP Express."
BASE COUNT   87 a   45 c   63 g   44 t
ORIGIN
Qy   1 GGCGGGCTTGTAAACAGTA 18
             ||||||||||||||||||
Db   162 GGCGGGCTTGTAAACAGT 178

Query Match   94.4%; Score 17; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 74;
Matches   17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
AW125499
LOCUS   AW125499   384 bp   mRNA   linear   EST 22-OCT-1999
DEFINITION UI-M-BH2.2-aqm-d-12-0-UI.s1 NIH_BMAP_M_S3.2 Mus musculus cDNA clone
            UI-M-BH2.2-aqm-d-12-0-UI 3', mRNA sequence.

```
ACCESSION   AW125499
VERSION     AW125499.1  GI:6101029
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 384)
AUTHORS     Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, USA
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized brain stems library cDNA Library Preparation: M.B.
            Soares Lab clone distribution: NIH BMAP cDNA clones will be made
            available by the means that is soon to be determined. When NIH
            determines the means for distribution of the BMAP cDNA clones, this
            record will be updated accordingly when that means, is determined.
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..384
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH2.2-aqm-d-12-0-UI"
                     /clone_lib="NIH_BMAP_M_S3.2"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S3.2 library is a subtracted library of a
                     series, ultimately derived from a mixture of individually
                     tagged normalized libraries from ten regions of the mouse
                     brain (cerebellum, brain stems, olfactory bulbs,
                     hypothalamus, cortex, amygdala, basal ganglia, pineal
                     gland, striatum, hippocampus) after a series of
                     subtractions to reduce the representation of cDNAs from
                     which ESTs had already been generated. The following
                     serially subtracted libraries were generated in this
                     process: NIH_BMAP_M_S2, NIH_BMAP_M_S1.
                     The subtracted library (NIH_BMAP_M_S3.2) was constructed
                     as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S2
                     clones from which 3 ESTs had been derived was used as a
                     driver in a hybridization with the NIH_BMAP_M_S2 library
                     in the form of single-stranded circles. The remaining
                     single-stranded circles (subtracted library) was purified
                     by hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (lifeTechnologies) to generate the
                     NIH_BMAP_M_S3.2 library. This procedure has been
                     previously described (Bonaldo, Lennon and Soares, Genome
                     Research 6:791-806 1996)
                     TAG_LIB=NIH_BMAP_M_S3.2
                     TAG_TISSUE=brain-stems
                     TAG_SEQ=TCAAG"
BASE COUNT       89 a      99 c      80 g      116 t
ORIGIN
Query Match             91.1%;   Score 16.4;  DB 10;  Length 384;
Best Local Similarity   94.4%;   Pred. No. 1.9e+02;
```

```
Matches   17;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy         1 GGCGGGCCTTGTAAACAGTA 18
             ||| |||||||||||||||||
Db       284 GGCAGCTTGTAAACAGTA 301
```

```
RESULT 8
LOCUS       AI465790/c                              451 bp   mRNA      linear   EST 09-MAR-1999
DEFINITION  vw97g05.y1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1262936 5' similar to gb:D31963 Mouse mRNA for cadherin-11
            (MOUSE);, mRNA sequence.
ACCESSION   AI465790
VERSION     AI465790.1  GI:4319820
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 451)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:665488
            This read is a RESEQUENCE of a previously sequenced mouse clone
            (correct orientation).
            This read has been verified (found to hit its original self in the
            correct orientation).
            Seq primer: ~40RP from Gibco
            High quality sequence stop: 349.
FEATURES             Location/Qualifiers
     source          1..451
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1262936"
                     /clone_lib="Soares_thymus_2NbMT"
                     /sex="male"
                     /tissue_type="thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed by a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCGCCGGCCGTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      137 a     107 c     107 g     100 t
ORIGIN
Query Match             91.1%;   Score 16.4;  DB 9;  Length 451;
Best Local Similarity   94.4%;   Pred. No. 2.1e+02;
Matches   17;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;
```

```
Qy         1 GGCGGGCCTTGTAAACAGTA 18
             ||| |||||||||||||||||
Db        68 GGCAGCTTGTAAACAGTA 51
```

```
RESULT 9
LOCUS       BG802493/c                              453 bp   mRNA      linear   EST 20-DEC-2001
DEFINITION  0181-71 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
            mRNA sequence.
```

ACCESSION   BG802493
VERSION   BG802493.1 GI:17949382
KEYWORDS   EST.
SOURCE   house mouse.
  Mus musculus
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 453)
  AUTHORS   Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
            White,R.A., Berenand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
  TITLE   Gene expression in the developing mouse retina by EST sequencing
            and microarray analysis
  JOURNAL   Nucleic Acids Res. 29 (24), 4983-4993 (2001)
  MEDLINE   21671825
COMMENT   Contact: Klein WH
            Department of Biochemistry and Molecular Biology
            University of Texas M.D. Anderson Cancer Center
            Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
            Tel: 713 792 3646
            Fax: 713 790 0329.
FEATURES   Location/Qualifiers
     source   1. .453
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone_lib="Mouse E14.5 retina lambda ZAP II Library"
                     /dev_stage="embryonic day 14.5 post-fertilization"
                     /tissue_type="neural retina"
                     /note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
                     Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps
                     (Manniatis); Cloning Technique: CUA Cloning (CloneAmp,
                     Life Technologies); Average insert size: 1.8 Kb;
                     Insertion site: TACGTCCACTGAATTCGAGTG--->. Other
                     information regarding entire library may be found at
                     http://pga.swmed.edu/Data/libraries/microarray_cdna_librar
                     ies.htm."
BASE COUNT   115 a   108 c   134 g   96 t
ORIGIN

Query Match   91.1%; Score 16.4; DB 12; Length 453;
Best Local Similarity   94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
             |||| |||||||||||||
Db   265 GGCAGCTTGTAAACAGTA 248

RESULT 10
LOCUS   BB854489/c
DEFINITION BB854489 RIKEN full-length enriched, B16 F10Y cells Mus musculus
            cDNA clone G37001H17 5', mRNA sequence.
ACCESSION   BB854489
VERSION   BB854489.1 GI:17095943
KEYWORDS   EST.
SOURCE   house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 455)
  AUTHORS   Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
            Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
            ,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
            , Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
            Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
            ,A., Takahashi,F., Takaku-Akahira,S., Tanaka,Y., Tomaru,A., Toya,T.
            , Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
  TITLE   RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
            2001)
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic

---

            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp.
            URL:http://genome.gsc.riken.go.jp/
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing Pipeline with 384 multicapillary sequencer. Genome Res.
            ,Y. and Hayashizaki,Y.
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y., 1757-1771 (2000)
            10 (11), 1757-1771 (2000)
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
            e mouse tissues.
FEATURES   Location/Qualifiers
     source   1. .455
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G37001H17"
                     /clone_lib="RIKEN full-length enriched, B16 F10Y cells"
                     /cell_type="B16 F10Y cells"
                     /note="pooled tissues ; (tissue_type=cerebellum,
                     dev_stage=16 days neonate, sex=mixed),
                     (tissue_type=cerebellum, dev_stage=0 day neonate,
                     sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
                     sex=male), (tissue_type=whole body, dev_stage=9 days
                     embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
                     embryo, sex=mixed)"
BASE COUNT   106 a   102 c   160 g   87 t
ORIGIN

Query Match   91.1%; Score 16.4; DB 10; Length 455;
Best Local Similarity   94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 GGCGGCTTGTAAACAGTA 18
             |||| |||||||||||||
Db   410 GGCAGCTTGTAAACAGTA 393

RESULT 11
LOCUS   BB854982/c
DEFINITION BB854982 RIKEN full-length enriched, B16 F10Y cells Mus musculus
            cDNA clone G370022B05 5', mRNA sequence.
ACCESSION   BB854982
VERSION   BB854982.1 GI:17096436
KEYWORDS   EST.
SOURCE   house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 479)
  AUTHORS   Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
            Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
            ,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
            , Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
            Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa

REFERENCE   1 (bases 1 to 498)
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
             Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
             Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
             ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
             ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
             Waterston,R. and Wilson,R.
TITLE   The WashU-NCI Mouse EST Project 1999
JOURNAL   Unpublished (1999)
COMMENT   Contact: Marra M/WashU-NCI Mouse EST Project 1999
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: mouseest@watson.wustl.edu
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             This clone, constructed by the IMAGE Consortium, was provided to
             This read is a RESEQUENCE of a previously sequenced mouse clone
             This read has been verified (found to hit its original self in the
             correct orientation)
             MGI:216404
             Seq primer: -40RP from Gibco
             High quality sequence stop: 481
             POLYA=No.

FEATURES   Location/Qualifiers
     source   1..498
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:335004"
                     /clone_lib="Soares mouse p3NMF19.5"
                     /dev_stage="19.5 dpc total fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCGCCCATTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA was kindly provided by
                     Dr. Minoru Ko (Wayne State University)."
BASE COUNT   123 a   110 c   160 g   105 t
ORIGIN

Qy   1 GGCGGCTTGTAAACAGTA 18
             ||| ||||||||||||||||
Db   324 GGCAGCTTGTAAACAGTA 307

RESULT 13
LOCUS   AA839644   501 bp   mRNA   linear   EST 27-FEB-1998
DEFINITION   vw97g05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
             IMAGE:1262936 5' similar to gb:D31963 Mouse mRNA for cadherin-11
             (MOUSE);, mRNA sequence.
ACCESSION   AA839644
VERSION   AA839644.1   GI:2915739
KEYWORDS   EST.
SOURCE   house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 501)
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., and
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

---

REFERENCE   1 (bases 1 to 479)
AUTHORS   Watahiki,A., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.
TITLE   RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
             2001)
JOURNAL   Unpublished (2001)
COMMENT   Contact: Yoshihide Hayashizaki
             Laboratory for Genome Exploration Research Group, RIKEN Genomic
             Sciences Center(GSC), Yokohama Institute
             The Institute of Physical and Chemical Research (RIKEN)
             1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
             Tel: 81-45-503-9222
             Fax: 81-45-503-9216
             Email: genome-res@gsc.riken.go.jp;
             URL:http://genome.gsc.riken.go.jp/;
             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
             ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new
             genes. Genome Res. 10 (10), 1617-1630 (2000)
             Watahiki,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
             wagi,K.,
             S. Kawai,J., Okazaki,Y., Ishikawa,T., Ozawa,R., Tanaka,T., Matsuura
             ,S., Yoneda,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
             Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer. Genome Res.
             10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
             ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
             encyclopedia: real-time sequence clustering for construction of a
             nonredundant cDNA library. Genome Res.. 11 (2), 281-289 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
             further details.
             e mouse tissues.

FEATURES   Location/Qualifiers
     source   1..479
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="3370022B05"
                     /clone_lib="RIKEN full-length enriched, B16 F10Y cells"
                     /cell_type="B16 F10Y cells"
                     /note="pooled tissues ; (tissue_type=cerebellum,
                     dev_stage=16 days neonate, sex=mixed),
                     (tissue_type=cerebellum, dev_stage=0 day neonate,
                     sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
                     sex=male), (tissue_type=whole body, dev_stage=9 days
                     embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
                     embryo, sex=mixed)"
BASE COUNT   135 a   98 c   145 g   101 t
ORIGIN

Qy   1 GGCGGCTTGTAAACAGTA 18
             ||| ||||||||||||||||
Db   323 GGCAGCTTGTAAACAGTA 306

RESULT 12
LOCUS   AI391334   498 bp   mRNA   linear   EST 15-MAR-2000
DEFINITION   mb72g07.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
             IMAGE:335004 5' similar to gb:X77557 M.musculus cad1 mRNA (MOUSE);,
             mRNA sequence.
ACCESSION   AI391334
VERSION   AI391334.1   GI:4217341
KEYWORDS   EST.
SOURCE   house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Qy   1 GGCGGCTTGTAAACAGTA 18
             ||| ||||||||||||||||
Db   324 GGCAGCTTGTAAACAGTA 307

Query Match   91.1%; Score 16.4; DB 9; Length 498;
Best Local Similarity   94.4%; Pred. No. 2.2e+02;
Matches   17; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Query Match   91.1%; Score 16.4; DB 10; Length 479;
Best Local Similarity   94.4%; Pred. No. 2.1e+02;
Matches   17; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

TITLE   Waterston,R.
JOURNAL   The Washu-HHMI Mouse EST Project
            Unpublished (1996)
COMMENT   Contact: Marra M/Mouse EST Project
            Washu-HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:665488
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 372.
FEATURES   Location/Qualifiers
     source   1..501
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1262936"
                     /clone_lib="Soares_thymus_2NbMT"
                     /sex="male"
                     /tissue_type="thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGACGACCGCCGCCGTTTTTTTTTTTTTTTTTTTTTTTTT
                     3'], double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT   152 a   119 c   119 g   111 t
ORIGIN

Qy 1 GGCGGCGCTTGTAAACAGTA 18
        |||||||||||||||||||
Db 68 GGCAGCTTGTAAACAGTA 51

Query Match   91.1%; Score 16.4; DB 9; Length 501;
Best Local Similarity   94.4%;   Pred. No. 2.2e+02;
Matches   17; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 14
LOCUS   BM934786/c
DEFINITION UI-M-BH2.2-aqm-d-12-0-UI.r1 NIH_BMAP_M_S3.2 Mus musculus cDNA clone
            UI-M-BH2.2-aqm-d-12-0-UI 5', mRNA sequence.
ACCESSION   BM934786   509 bp   mRNA   linear   EST 13-MAR-2002
VERSION   BM934786.1 GI:1939938
KEYWORDS   EST.
SOURCE   house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 509)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE   Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
COMMENT   Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov

COMMENT   cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            The following repetitive elements were found in this cDNA
            sequence: 486-507, >POLY_A#Simple_repeat
            Seq primer: M13 REVERSE
FEATURES   Location/Qualifiers
     source   1..509
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH2.2-aqm-d-12-0-UI"
                     /clone_lib="NIH_BMAP_M_S3.2"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S3.2 library is a subtracted library of a
                     series, ultimately derived from a mixture of individually
                     tagged normalized libraries from ten regions of the mouse
                     brain (cerebellum, brain stems, olfactory bulbs,
                     hypothalamus, cortex, amygdala, basal ganglia, pineal
                     gland, striatum, hippocampus) after a series of
                     subtractions to reduce the representation of cDNAs from
                     which ESTs had already been generated. The following
                     serially subtracted libraries were generated in this
                     process: NIH_BMAP_M_S2, NIH_BMAP_M_S1.
                     The subtracted library (NIH_BMAP_M_S3.2) was constructed
                     as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S2
                     clones from which 3' ESTs had been derived was used as a
                     driver in a hybridization with the NIH_BMAP_M_S2 library
                     in the form of single-stranded circles. The remaining
                     single-stranded circles (subtracted library) was purified
                     by hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (LifeTechnologies) to generate the
                     NIH_BMAP_M_S3.2 library. This procedure has been
                     previously described (Bonaldo, Lennon and Soares, Genome
                     Research 6:791-806, 1996)."
BASE COUNT   151 a   106 c   135 g   117 t
ORIGIN

Qy 1 GGCGGCGCTTGTAAACAGTA 18
        |||||||||||||||||||
Db 219 GGCAGC...AACAGTA 202

Query Match   91.1%; Score 16.4; DB 14; Length 509;
Best Local Similarity   94.4%;   Pred. No. 2.2e+02;
Matches   17; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 15
LOCUS   BF464496
DEFINITION UI-M-CG0p-bpz-c-07-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
            UI-M-CG0p-bpz-c-07-0-UI 3', mRNA sequence.
ACCESSION   BF464496   539 bp   mRNA   linear   EST 04-DEC-2000
VERSION   BF464496.1 GI:11533679
KEYWORDS   EST.
SOURCE   house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 539)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE   Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
COMMENT   Contact: Chin, H
            National Institute of Mental Health

```
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA=No.
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FEATURES   Location/Qualifiers
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                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="UI-M-CG0p-bpz-c-07-0-UI"
                  /clone_lib="NIH_BMAP_Ret4_S2"
                  /lab_host="DH10B (Life Technologies)"
                  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                  polylinker; Site_1: Not I; Site_2: Eco RI; The
                  NIH_BMAP_Ret4_S2 library is a subtracted library,
                  ultimately derived from mouse retina tissue libraries at
                  various stages of development. For a detailed description
                  of the library from which this clone was derived, please
                  visit our web site at brainest.eng.ulowa.edu. The tissue
                  for this library was contributed by Dr. Xin-Yuan Fu, Yale
                  University School of Medicine

BASE COUNT   121 a   158 c   124 g   136 t
ORIGIN   TAG_SEQ=None found"

Qy   1 GGCGGCTTGTAAACAGTA 18
         ||| |||||||||||||||
Db   295 GGCAGCTTGTAAACAGTA 312

Query Match   91.1%;   Score 16.4; DB 12;   Length 539;
Best Local Similarity 94.4%;   Pred. No. 2.2e+02;
Matches   17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: June 22, 2003, 09:13:30
Job time : 1761 secs